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Remarks:

- The applicant has subsequently filed a sequence listing and declared, that it includes no new matter.
- Claims 11 to 12 are deemed to be abandoned due to non-payment of the claims fees (Rule 31 (2) EPC).

(54) **Gastric helicobacter 16 S rDNA sequences from cattle and pigs and their use for detection and typing of Helicobacter strains**

(57) The present invention relates to new *Helicobacter* 16S rRNA or rDNA polynucleotide sequences useful for detection and typing of *Helicobacter* infected human and animal samples. The present invention relates more particularly to new "*Candidatus Helicobacter bovis*" and "*Candidatus Helicobacter suis*" sequences

as defined in SEQ ID NO 1 and 2, sequence variants and fragments thereof. These new *Helicobacter* sequences allow the design of sequence specific probes and primers for detection and typing of the strains they are derived from. Diagnostic methods and kits employing such new bovine and porcine *Helicobacter* sequences are also disclosed.

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Description

[0001] The present invention relates to the field of detection and typing of *Helicobacter* infection in clinical samples from humans and other mammals. The present invention relates more particularly to bovine and porcine 16 rDNA polynucleotide sequences as well as their use in diagnostic applications.

[0002] In the 19th century, gastric spiral organisms were described for the first time in different animals (Rappin, 1881; Bizzozero, 1893; Salomon, 1896). Salomon observed spiral organisms in the stomachs of dogs, cats and the brown Norwegian rat but not in humans, monkeys, pigs, mice, pigeons, crows and cattle (Salomon, 1896). It was only in 1984 that a renewed interest emerged for similar organisms after the isolation of *Helicobacter pylori* from the human stomach (Marshall & Warren, 1984). The association of *H. pylori* with chronic gastritis, peptic ulceration and gastric cancer (Cover & Blaser, 1992; Blaser et al., 1991; Parsonnet et al., 1991) resulted in intensive research worldwide. Various *Helicobacter* species were isolated from the gastrointestinal tract of different animals. To date, the genus *Helicobacter* consists of 18 different species (On, 1996; Franklin et al., 1996; Mendes et al., 1996; Jalava et al., 1997; Trivett-Moore et al., 1997; Shen et al., 1997) and constitutes together with the genera *Wolinella*, *Campylobacter* and *Arcobacter*, the epsilon subdivision of the *Proteobacteria*, also known as rRNA superfamily VI (Vandamme et al., 1991).

[0003] In 1992, two different groups almost simultaneously reported the presence of helically shaped bacteria in the abomasum of calves and adult cattle based on histological data (Günther & Schulze, 1992; Haringsma & Mouwen, 1992). Both groups described large numbers of spiral-shaped bacteria in the gastric crypts of the pyloric region and considered them as putative *Helicobacter* species. Further indirect evidence of the presence of *Helicobacter-like* organisms in adult cattle and calves was given by serological studies. Seidel et al. (1996) found significant titers of antibodies against *H. pylori* epitopes in the serum of calves after absorption with *Campylobacter jejuni*, *Wolinella succinogenes*, *Escherichia coli* and *Proteus mirabilis* strains. One report described a bactericidal activity of bovine serum, colostrum and milk against *H. pylori* (Korhonen et al., 1995). In vitro isolation of these organisms has not been successful so far (Jelinski et al., 1995; Braun et al., 1997) and the taxonomic status of these putative *Helicobacter-like* bacteria is unknown.

[0004] The pathogenic role of *H. pylori* led to speculations about the association of bovine *Helicobacter-like* bacteria with abomasal ulcer disease, although no conclusive evidence has been provided to date (Günther & Schulze, 1992; Haringsma & Mouwen, 1992). Other bacteria such as *Campylobacter* species and *Clostridium perfringens* have also been studied in association with the occurrence of abomasal lesions (Al Mashat & Taylor, 1980; Mills et al., 1990; Jelinski et al., 1995).

[0005] Within the genus *Helicobacter*, a phylogenetic subgroup of morphologically similar bacteria can be distinguished. These bacteria, characterized by their long and tightly coiled (gastrospirillum-like) appearance, have been observed in gastric biopsies of humans, cats, lemurs, dogs, pigs and exotic carnivores (Dent et al., 1987; Lee et al., 1988; O'Rourke et al., 1992; Hänninen et al., 1996; Jalava et al., 1997; Queiroz et al., 1990; Eaton et al., 1993; Jakob et al., 1997). Three species with this morphology (*H. felis*, *H. bizzozeronii*, *H. salomonis*) have been isolated and characterised from gastric samples of cats and dogs (Paster et al., 1991; Hänninen et al., 1996; Jalava et al., 1997).

[0006] The observation of gastrospirillum-like organisms in humans was described for the first time in 1987 by Dent et al (Dent et al., 1987). Although initially referred to as "*Gastrospirillum hominis*" (McNulty et al., 1989), this organism was later renamed "*Helicobacter heilmannii*" as 16S rDNA sequence analysis revealed that these human gastrospirilla belonged to the genus *Helicobacter* (O'Rourke et al., 1992; Solnick et al., 1993). From these results, it also became clear that there were at least two different types of "*Helicobacter heilmannii*", referred to as type 1 and type 2. This observation was based on a 3.5 % sequence difference, suggesting that the two sequences represented two different species. The first isolation of a "*Helicobacter heilmannii*" - like bacterium from humans was recently reported by Andersen et al. (1996).

[0007] In pigs, gastrospirillum-like bacteria were observed in the antral pits and at the mucosal surface of the stomach (Queiroz et al., 1990) and have provisionally been named "*Gastrospirillum suis*" (Mendes et al., 1990). Histopathological studies associated this bacterium with pyloric lymphonodular gastritis (Mendes et al., 1991) and gastric ulcer disease of the pars oesophagea in pigs (Barbosa et al., 1995; Queiroz et al., 1996). Although *in vitro* cultivation of "*Gastrospirillum suis*" has been unsuccessful (Queiroz et al., 1990), *in vivo* cultivation in mice and rats has been reported (Moura et al., 1993; Mendes et al., 1996). In one case, a *Helicobacter* was isolated from the faeces of swine (Seymour et al., 1994) which was later characterised as *Helicobacter pametensis* (Dewhirst et al., 1994). Other members of rRNA superfamily VI, *Campylobacter hyointestinalis* subsp. *Lawsonii* (On et al., 1995), *Arcobacter butzleri* and *Arcobacter cryaerophilus* (Suarez et al., 1997), have also been isolated from the stomach of swine.

[0008] As "*Gastrospirillum suis*" remains unculturable, an official species designation is impossible according to the guidelines of the *International Code of Nomenclature of Bacteria* which are stating the necessity of a broad range of phenotypic and phylogenetic data. Murray and Schleifer (1994) anticipated this problem, and proposed a provisional status to record the properties of putative taxa of prokaryotes. This proposal was implemented in 1995 by the International Committee on Systematic Bacteriology by the introduction of the provisional status *Candidatus* for the description

of uncultivable organisms based upon genomic data and to a certain extent structural, metabolic, reproductive and environmental characteristics (Murray and Stackebrandt, 1995).

[0009] It is an aim of the present invention to provide new *Helicobacter* nucleotide sequences of the 16S rRNA coding gene.

[0010] It is also an aim of the present invention to provide new probes and primers for detection of *Helicobacter* species.

[0011] It is also an aim of the present invention to provide methods and kits for detection and/or typing of *Helicobacter* species present in cattle and pigs.

[0012] It is further an aim of the present invention to provide methods and kits for detection of zoönoses in human samples.

[0013] It is also an aim of the present invention to provide new nucleotide sequences for studying and detecting the occurrence of pathogenic *Helicobacter* strains in mammals, more particularly in cattle and pigs.

[0014] All the aims of the present invention are met by the following embodiments.

[0015] According to one embodiment, the present invention relates to an isolated 16S rDNA *Helicobacter* polynucleic acid sequence selected from any of the following

(a) a sequence represented in any of SEQ ID NO 1 or 2, or the RNA version thereof,

(b) a sequence which hybridizes under stringent conditions to any of the sequences set out in (a).

[0016] The term "16S ribosomal polynucleic acid sequences" as used in the present invention refers to 16S rRNA or 16S rDNA polynucleic acid sequences.

[0017] According to a first aspect of the present invention, seven abomasal biopsies of adult cattle were sampled from different Belgian and Dutch farms. In all samples the presence of *Helicobacter*-like organisms was demonstrated by biochemical, immunohistochemical and electronmicroscopical data. Bacterial 16S rDNA was amplified from each sample by PCR and sequences were determined either by direct or indirect sequence analysis. Pairwise comparisons revealed all sequences to be more than 99 % homologous. Phylogenetic analysis placed the organism, corresponding to the reference sequence R2XA, within the genus *Helicobacter*. A diagnostic PCR-assay was designed, differentiating the bovine 16S rDNA sequences from those of 15 different *Helicobacter* strains and *Wolinella succinogenes*. These results indicated the corresponding organism to represent a single taxon. The low similarity level towards *H. bilis* (92.8 %), its closest validly named neighbour, strongly suggests that this novel taxon indeed is a novel *Helicobacter* species. An *in situ* hybridisation procedure associated the bovine sequences to the *Helicobacter*-like organisms in the abomasum.

[0018] According to a second aspect, the present invention relates to new *Helicobacter* sequences from pigs. Stomachs of five slaughterhouse pigs originating from different Belgian and Dutch farms were selected based on the presence of "*Gastrospirillum suis*"-like bacteria as demonstrated by biochemical, immunohistochemical and electronmicroscopical data. Using broad range primers, bacterial 16S rDNA was amplified by PCR and five *Helicobacter*-like sequences were determined either by direct or indirect sequence analysis. An intersequence homology of 99.7 % was observed, suggesting that the sequences originated from strains belonging to a single species. Phylogenetic analysis of the consensus sequence placed the organism within the genus *Helicobacter*, where it formed a distinct subgroup together with other gastrospirillum-like bacteria (*H. felis*, *H. bizzozeronii*, *H. salomonis*, "*H. heilmannii*" type 1 and type 2). Diagnostic PCR-primers and a probe were developed, differentiating the porcine sequences from all known *Helicobacters*. These results indicate that the porcine sequences represent a single taxon within the genus *Helicobacter*. The low similarity level towards *H. salomonis* (96.6 %), its closest validly named neighbour, strongly suggests that this novel taxon indeed is a novel *Helicobacter* species. *In situ* hybridisation experiments linked the reference sequence to the "*Gastrospirillum suis*"-like bacteria. On the basis of these results, the name "*Candidatus Helicobacter suis*" for this new gastric *Helicobacter* from pigs is proposed.

[0019] These sequences are commonly characterized by the fact that they can be used to study and most probably detect pathogenic *Helicobacter* strains in mammals, more particularly in cattle and pigs. Such pathogenic strains cause for instance gastric ulcers and chronic gastritis.

[0020] The present invention relates more particularly to an isolated polynucleic acid sequence as defined above represented by any of SEQ ID NO 1 or 2 or 15 to 24.

[0021] The present invention also relates to an isolated polynucleic acid sequence as defined above which is more than 92.8%, preferably more than 93.5%, more preferably more than 95% and most preferably more than 97.5% homologous to SEQ ID NO 1. Other preferred ranges of homology include 93, 94, 94.5, 95.5, 96, 96.5, 97, 98, 98.5, 99 or 99.5%.

[0022] Sequences which have a homology of more than 92.8% to SEQ ID NO 1 are considered to belong to the same group of organisms as the one where SEQ ID NO 1 has been derived from.

[0023] According to the present invention, the homologies of SEQ ID NO 1 were calculated by means of the GENSCAN program (Applied Maths bvba, Risquons-toutstraat 38, B-8511 Kortrijk, Belgium).

[0024] The term "homology" refers to a sequence identity as calculated by the above-given program.

[0025] SEQ ID NO 2 is 99.5% homologous to the closest found sequence. Sequences of more than 99.5% homology compared to SEQ ID NO 2 are also within the scope of the present invention.

[0026] Preferred sequences according to the present invention are set out in Figures 1, 2, 4 and 5: SEQ ID NO 1 to 2 and 15 to 24. Also unique parts and fragments of these sequences are part of the present invention. Preferred unique parts are set out in Table 2.

[0027] Since SEQ ID NO 2 shows 96.6% homology to its closest found validly named neighbour, the use of sequences of more than 96.6% homology to SEQ ID NO 1 for identification or typing of *Helicobacter* species is also within the scope of the present invention. Preferably sequences of more than 97%, 97.5%, 98%, 98.5%, 99% or 99.5% homology to SEQ ID NO 2 are used for this goal.

[0028] According to another embodiment, the present invention relates to a part of an isolated polynucleic acid as defined above, more particularly part or a fragment of SEQ ID NO 1 or 2, wherein said part is unique to the polynucleic acid sequence it is derived from.

[0029] According to the present invention, the term "unique" implies that at least one nucleotide of the fragment or part is different from a nucleotide present at the same nucleotide position in a known 16S rRNA sequence or the corresponding gene. Such a nucleotide can be deduced theoretically by looking at an alignment of the new sequences of this invention with other closely related *Helicobacter* 16S rDNA gene nucleotide sequences (see Figures 1, 2, 4 and 5). Said type of nucleotides are unique to the sequence they are derived from. These fragments are thus not part of any known 16S rRNA or gene sequence encoding the same. The fragments according to this embodiment of the present invention may be of any length between 10 to the maximum number of nucleotides of SEQ ID NO 1 or 2 or its variants. Preferred lengths are 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, etc. nucleotides.

[0030] According to another embodiment, the present invention relates to a probe which specifically hybridizes to a polynucleic acid sequence as defined above.

[0031] Preferred probes are given in Table 2. Probe *R628f* is a preferred "*Candidatus Helicobacter bovis*" specific probe. Probe *V100f* is a preferred "*Candidatus Helicobacter suis*" specific probe. Other suitable probes may be derived from a visual inspection of the alignment shown in Figure 1 or 2.

[0032] According to another embodiment, the present invention relates to a primer which specifically amplifies a polynucleic acid sequence as defined above.

[0033] Preferred primers according to the present invention are given in Table 2. Primers *R574f* and *R832r* are preferred "*Candidatus Helicobacter bovis*" specific primers and are suited for a specific PCR and in situ hybridisation assays. Primers *V832f* and *V1621r* are preferred "*Candidatus Helicobacter suis*" specific primers for a specific PCR and in situ hybridisation assays. Other suitable primers according to the present invention may be derived from a visual inspection of the alignment shown in Figure 1 or 2.

[0034] Relying on the principles well known in the art, the skilled man will be able to select primers that allow specific amplification of SEQ ID NO 1 or 2 or the claimed variants thereof under given or experimental conditions, such as temperature, buffer composition, polymerase chain reaction cycle etc. Likewise the skilled man will be able to select probes that specifically hybridize to either SEQ ID NO 1 or 2 or the claimed variants under given experimental conditions such as temperature, buffer composition etc. Having chosen primers and/or probes, the skilled man will furthermore be able to assess the efficacy of these primers or probes without undue experimentation. It is also obvious that the skilled man may choose to combine more than one primer pair or more than one probe to carry out the method defined above.

[0035] In some cases, one may not wish to detect all SEQ ID NO 1 or 2 variants as specified above, for instance if one intends to detect alleles found in a certain geographic region.

[0036] According to another embodiment, the present invention relates to a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising hybridizing the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one probe as defined above.

[0037] Preferably said method may be used to study and detect the occurrence of pathogenic *Helicobacter* strains.

[0038] According to another embodiment, the present invention relates to a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically amplifying the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one primer as defined above.

[0039] Preferably said method may be used to study and detect the occurrence of pathogenic *Helicobacter* strains.

[0040] A preferred embodiment according to the present invention involves a method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising first amplifying a specific target region encompassed in or comprising the 16S rRNA region of said *Helicobacter* strains present in said biological sample and subsequently hybridizing the 16S rRNA or 16S rDNA target region polynucleotides of said *Helicobacter* strains present in said bio-

logical sample with at least one (or more than one) probe as defined above.

[0041] Different techniques can be applied to perform the methods of the present invention. These techniques may comprise immobilizing the target polynucleic acids, possibly after amplification, on a solid support and performing a hybridization with labelled oligonucleotide probes of the present invention. Alternatively, said probes may be immobilized on a solid support and hybridization may be performed with labelled target polynucleic acids, possibly after amplification (i.e. a reverse hybridization).

[0042] A preferred method according to the present invention is an *in situ* hybridisation assay (see Examples section).

[0043] The well-known technique of Southern blotting is one example of a hybridization assay that can be used to perform the methods of the present invention. Another example of a hybridization technique is the DNA enzyme immuno assay (DEIA). According to this method, PCR products are generated by a primer set, of which either the forward or the reverse primer contain biotin at the 5' end. This allows binding of the biotinylated amplimers to streptavidin-coated microtiter wells. PCR products are denatured by sodium hydroxide, which allows removal of the non-biotinylated strand. Specific digoxigenin (DIG)-labelled oligonucleotide probes are hybridized to the single-stranded immobilized PCR product and hybrids are detected by enzyme-labelled conjugate and colorimetric methods.

[0044] A convenient reverse hybridization technique is the LiPA assay. The LiPA uses oligonucleotide probes immobilized as parallel lines on a solid support strip (Stuyver et al. 1993; international patent application WO 94/12670). This approach is particularly advantageous since it is fast and simple to perform.

[0045] It is to be understood that any other type of hybridization assay or hybridization format using any of the selected probes as described further in the invention, is also covered by the present invention.

[0046] According to another embodiment, the present invention relates to a diagnostic kit for detection and/or typing of *Helicobacter* strains comprising:

- at least one probe as defined above and/or,

- at least one primer as defined above.

[0047] According to another embodiment, the present invention relates to a medicament comprising a polynucleic acid sequence as defined above.

[0048] According to another embodiment, the present invention relates to a polynucleic acid sequence as defined above for use as a medicament.

[0049] The following definitions and explanations will permit a better understanding of the present invention.

[0050] The target material in the samples to be analysed may either be DNA or RNA, e.g. genomic DNA, messenger RNA, viral RNA or amplified versions thereof. These molecules are in this application also termed "polynucleic acids" or "polynucleotides". More particularly, the target material according to the present invention will be 16S ribosomal RNA or DNA or amplified versions thereof.

[0051] Well-known extraction and purification procedures are available for the isolation of RNA or DNA from a sample (e.g. in Sambrook et al., 1989).

[0052] The term "probe" according to the present invention refers to a single-stranded oligonucleotide which is designed to specifically hybridize to "*Candidatus Helicobacter bovis* or *suis*" polynucleic acids.

[0053] The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. The length and the sequence of the primer must be such that they allow to prime the synthesis of the extension products. Preferably the primer is about 5-50 nucleotides long. Specific length and sequence will depend on the complexity of the required DNA or RNA targets, as well as on the conditions at which the primer is used, such as temperature and ionic strength. It is to be understood that the primers of the present invention may be used as probes and *vice versa*, provided that the experimental conditions are adapted.

[0054] The expression "suitable primer pair" in this invention refers to a pair of primers allowing specific amplification of a "*Candidatus Helicobacter bovis* or *suis*" polynucleic acid fragment.

[0055] The term "target region" of a probe or a primer according to the present invention is a sequence within the "*Candidatus Helicobacter bovis* or *suis*" polynucleic acids to which the probe or the primer is completely complementary or partially complementary (i.e. with some degree of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

[0056] "Specific hybridization" of a probe to a target region of respectively the "*Candidatus Helicobacter bovis*" or "*Candidatus Helicobacter suis*" polynucleic acids means that said probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions said probe does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

[0057] "Specific hybridization" of a primer to a target region of respectively the "*Candidatus Helicobacter bovis*" or "*Candidatus Helicobacter suis*" polynucleic acids means that, during the amplification step, said primer forms a duplex

with part of this region or with the entire region under the experimental conditions used, and that under those conditions said primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

[0058] "Specific amplification" of a fragment of respectively the "*Candidatus Helicobacter bovis*" or "*Candidatus Helicobacter suis*" polynucleic acids means amplification of the fragment for which the primers were designed, and not of any other fragment of the polynucleic acids present in a sample.

[0059] The fact that amplification primers do not have to match exactly with the corresponding target sequence in the template to warrant proper amplification is amply documented in the literature (Kwok et al., 1990). However, when the primers are not completely complementary to their target sequence, it should be taken into account that the amplified fragments will have the sequence of the primers and not of the target sequence. Primers may be labelled with a label of choice (e.g. biotine). The amplification method used can be either polymerase chain reaction (PCR; Saiki et al., 1988), ligase chain reaction (LCR; Landgren et al., 1988; Wu & Wallace, 1989; Barany, 1991), nucleic acid sequence-based amplification (NASBA; Guatelli et al., 1990; Compton, 1991), transcription-based amplification system (TAS; Kwoh et al., 1989), strand displacement amplification (SDA; Duck, 1990) or amplification by means of Q β replicase (Lomeli et al., 1989) or any other suitable method to amplify nucleic acid molecules known in the art.

[0060] Preferably, the probes of the invention are about 5 to 50 nucleotides long, more preferably from about 10 to 25 nucleotides. Particularly preferred lengths of probes include 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics.

[0061] Probe and primer sequences are represented throughout the specification as single stranded DNA oligonucleotides from the 5' to the 3' end. It is obvious to the man skilled in the art that any of the below-specified probes can be used as such, or in their complementary form, or in their RNA form (wherein T is replaced by U).

[0062] The probes according to the invention can be prepared by cloning of recombinant plasmids containing inserts including the corresponding nucleotide sequences, if need be by excision of the latter from the cloned plasmids by use of the adequate nucleases and recovering them, e.g. by fractionation according to molecular weight. The probes according to the present invention can also be synthesized chemically, for instance by the conventional phospho-triester method.

[0063] The oligonucleotides used as primers or probes may also comprise nucleotide analogues such as phosphorothiates (Matsukura et al., 1987), alkylphosphorothiates (Miller et al., 1979) or peptide nucleic acids (Nielsen et al., 1991; Nielsen et al., 1993) or may contain intercalating agents (Asseline et al., 1984). As most other variations or modifications introduced into the original DNA sequences of the invention these variations will necessitate adaptations with respect to the conditions under which the oligonucleotide should be used to obtain the required specificity and sensitivity. However, the eventual results of hybridization will be essentially the same as those obtained with the unmodified oligonucleotides. The introduction of these modifications may be advantageous in order to positively influence characteristics such as hybridization kinetics, reversibility of the hybrid-formation, biological stability of the oligonucleotide molecules, etc.

[0064] The term "solid support" can refer to any substrate to which an oligonucleotide probe can be coupled, provided that it retains its hybridization characteristics and provided that the background level of hybridization remains low. Usually the solid substrate will be a microtiter plate, a membrane (e.g. nylon or nitrocellulose) or a microsphere (bead) or a chip. Prior to application to the membrane or fixation it may be convenient to modify the nucleic acid probe in order to facilitate fixation or improve the hybridization efficiency. Such modifications may encompass homopolymer tailing, coupling with different reactive groups such as aliphatic groups, NH₂ groups, SH groups, carboxylic groups, or coupling with biotin, haptens or proteins.

[0065] The term "labelled" refers to the use of labelled nucleic acids. Labelling may be carried out by the use of labelled nucleotides incorporated during the polymerase step of the amplification such as illustrated by Saiki et al. (1988) or Bej et al. (1990) or labelled primers, or by any other method known to the person skilled in the art. The nature of the label may be isotopic (³²P, ³⁵S, etc.) or non-isotopic (biotin, digoxigenin, etc.).

[0066] The "biological sample" may be for instance cultured *Helicobacter* strains, gastric, abomasal stomachs, omasal stomachs, reticulum and rumen, or duodenal biopsies (fresh or paraffine material), faeces, saliva, mouth mucosa, gastric juice or urine. Preferably these samples may be taken from piglets, pigs, humans, calves, cattle, etc.

[0067] For designing probes with desired characteristics, the following useful guidelines known to the person skilled in the art can be applied.

[0068] Because the extent and specificity of hybridization reactions such as those described herein are affected by a number of factors, manipulation of one or more of those factors will determine the exact sensitivity and specificity of a particular probe, whether perfectly complementary to its target or not. The importance and effect of various assay conditions are explained further herein.

[0069] **The stability of the [probe : target] nucleic acid hybrid should be chosen to be compatible with the assay

conditions. This may be accomplished by avoiding long AT-rich sequences, by terminating the hybrids with G:C base pairs, and by designing the probe with an appropriate T_m . The beginning and end points of the probe should be chosen so that the length and %GC result in a T_m about 2-10°C higher than the temperature at which the final assay will be performed. The base composition of the probe is significant because G-C base pairs exhibit greater thermal stability as compared to A-T base pairs due to additional hydrogen bonding. Thus, hybridization involving complementary nucleic acids of higher G-C content will be more stable at higher temperatures.

[0070] **Conditions such as ionic strength and incubation temperature under which a probe will be used should also be taken into account when designing a probe. It is known that the degree of hybridization will increase as the ionic strength of the reaction mixture increases, and that the thermal stability of the hybrids will increase with increasing ionic strength. On the other hand, chemical reagents, such as formamide, urea, DMSO and alcohols, which disrupt hydrogen bonds, will increase the stringency of hybridization. Destabilization of the hydrogen bonds by such reagents can greatly reduce the T_m . In general, optimal hybridization for synthetic oligonucleotide probes of about 10-50 bases in length occurs approximately 5°C below the melting temperature for a given duplex. Incubation at temperatures below the optimum may allow mismatched base sequences to hybridize and can therefore result in reduced specificity.

[0071] **It is desirable to have probes which hybridize only under conditions of high stringency. Under high stringency conditions only highly complementary nucleic acid hybrids will form; hybrids without a sufficient degree of complementarity will not form. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands forming a hybrid. The degree of stringency is chosen such as to maximize the difference in stability between the hybrid formed with the target and the non-target nucleic acid.

[0072] **Regions in the target DNA or RNA which are known to form strong internal structures inhibitory to hybridization are less preferred. Likewise, probes with extensive self-complementarity should be avoided. As explained above, hybridization is the association of two single strands of complementary nucleic acids to form a hydrogen bonded double strand. It is implicit that if one of the two strands is wholly or partially involved in a hybrid that it will be less able to participate in formation of a new hybrid. There can be intramolecular and intermolecular hybrids formed within the molecules of one type of probe if there is sufficient self complementarity. Such structures can be avoided through careful probe design. By designing a probe so that a substantial portion of the sequence of interest is single stranded, the rate and extent of hybridization may be greatly increased. Computer programs are available to search for this type of interaction. However, in certain instances, it may not be possible to avoid this type of interaction.

[0073] **Standard hybridization and wash conditions are disclosed in the Examples section. Other conditions are for instance 3X SSC (Sodium Saline Citrate), 20% deionized FA (Formamide) at 50°C. Other solutions (SSPE (Sodium saline phosphate EDTA), TMAC (Tetramethyl ammonium Chloride), etc.) and temperatures can also be used provided that the specificity and sensitivity of the probes is maintained. When needed, slight modifications of the probes in length or in sequence have to be carried out to maintain the specificity and sensitivity required under the given circumstances.

[0074] The term "hybridization buffer" means a buffer allowing a hybridization reaction between the probes and the polynucleic acids present in the sample, or the amplified products, under the appropriate stringency conditions.

[0075] The term "wash solution" means a solution enabling washing of the hybrids formed under the appropriate stringency conditions.

[0076] The Examples as set out below only serve to illustrate the present invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

[0077]

Figure 1 represents an alignment of the reference sequence R2XA of "*Candidatus Helicobacter bovis*" (SEQ ID NO 1) with sequences of strains belonging to the epsilon subdivision (Table 3) which were retrieved from the EMBL data library and were aligned with reference sequence R2XA

Figure 2 represents an alignment of the reference sequence V2BXA of "*Candidatus Helicobacter suis*" (SEQ ID NO 2) sequence with the sequences of strains belonging to the same phylogenetic lineage (Table 3).

Figure 3A represents a phylogenetic tree based on the phylogenetic analysis of "*Candidatus Helicobacter bovis*" as set out in the Examples section. The scale bar represents a one % difference in nucleotide sequences as determined by measuring the length of horizontal lines connecting any two species.

Figure 3B represents a phylogenetic tree based on the phylogenetic analysis of "*Candidatus Helicobacter suis*" as set out in the Examples section. The scale bar represents a one % difference in nucleotide sequences as determined by measuring the length of horizontal lines connecting any two species.

Figure 4 represents an alignment of the different "*Candidatus Helicobacter bovis*" sequences. The reference sequence is R2XA001 (SEQ ID NO 1). The other sequences are R5XE001 (SEQ ID NO 15), R3XA001 (SEQ ID NO 16), R6XA001 (SEQ ID NO 17), R13D001INV (SEQ ID NO 18), R27TOTAAL (SEQ ID NO 19) and R28TOTAAL (SEQ ID NO 20).

Figure 5 represents an alignment of the different "*Candidatus Helicobacter suis*" sequences. The reference sequence is RBXA001 (SEQ ID NO 2). The other sequences are 4AXA001 (SEQ ID NO 21), 6W06001 (SEQ ID NO 22), V14D001 (SEQ ID NO 23), V19DINV001 (SEQ ID NO 24).

EXAMPLES

Material and Methods

Samples from cattle

[0078] Seven abomasal stomachs from clinically healthy slaughterhouse cattle originating from different Belgian and Dutch farms, were selected. The stomachs were opened longitudinally along the greater curvatura and rinsed gently with tap water. Two small mucosal fragments were taken from each stomach, one near the torus pyloricus and one in the fundic region, and were tested for urease activity (CUTest, Temmler Pharma) for h at 37 °C. Three mucosal biopsies from the pyloric region were taken for immunohistochemistry and *in situ* hybridisation and placed into 4 % buffered formaline for 24 hours. For electronmicroscopy, a pyloric sample was taken from the same region and fixed in cacodylate buffer (0.1 M, pH 7.0) containing 5 % glutaraldehyde and 0.15 % (wt/vol) ruthenium red. From each stomach a mucosal fragment was also taken for PCR analysis, placed into sterile PBS and frozen in liquid nitrogen. Special care was taken during sampling to avoid cross-contamination.

Samples from pigs

[0079] Stomachs from 5 healthy slaughterhouse pigs were selected, all originating from different farms in Belgium and the Netherlands. The stomachs were opened longitudinally along the greater curvatura and rinsed gently with tap water. A small mucosal fragment was taken from each stomach near the torus pyloricus and placed into an urease test tube (CUTest, Temmler Pharma) for 2 hours at 37 °C. Mucosal biopsies from the antral part of the stomach were taken along the curvatura major ($n=2$) and the curvatura minor ($n=2$) for immunohistochemical evaluation and placed into 4 % buffered formalin. For electronmicroscopy, samples were taken from the same places and fixed in 0.1 M cacodylate buffer (pH 7.0) containing 5% glutaraldehyde and 0.15 % (wt/vol) ruthenium red. Of each stomach a mucosal fragment was also taken for PCR, placed into sterile PBS and frozen in liquid nitrogen. Special care was taken during sampling to avoid cross-contamination.

Reference strains for "*Candidatus Helicobacter bovis*"

[0080] A total of 15 *Helicobacter* strains and 1 *Wolinella succinogenes* strain were used to test the specificity of the "*Candidatus Helicobacter bovis*" specific PCR (Table 1). Strains were grown on a 5 % Mueller-Hinton blood agar and incubated at 37 °C in a microaerophilic atmosphere containing approximately 5 % O₂, 3.5 % CO₂, 7.5 % H₂ and 84 % N₂. Bacteriological purity was checked by plating and Gram-staining.

Reference strains for "*Candidatus Helicobacter suis*"

[0081] A total of 15 *Helicobacter* strains were used to test the specificity of the "*Candidatus Helicobacter suis*"-specific PCR assay (Table 1). Strains were grown on a 5% Mueller-Hinton blood agar and incubated at 37 °C in a microaerobic atmosphere containing approximately 5 % O₂, 3.5 % CO₂, 7.5 % H₂ and 84 % N₂. Bacteriological purity was checked by plating and Gram-staining.

Immunohistochemistry

[0082] Immunohistochemical staining was performed to assess the presence of *Helicobacter*-like organisms. Formalin-fixed samples were dehydrated and paraffin-embedded. Sections of 4 µm were made of the paraffin-embedded tissues and were placed on 3-aminopropyltriethoxysilane-coated slides (APES, Sigma-Aldrich) and dried overnight at 60 °C. After dewaxing with xylene and rehydration in graded series with ethanol and distilled water, sections were placed in citrate buffer (0.1M with 2% ureum) and were boiled (1 x 3 min, 2 x 5 min) in a 800 Watt microwave oven

(Whirlpool M611) to elicit antigen retrieval. Slides were then incubated with 12 % hydrogenperoxide in methanol (30 min) in order to block endogenous peroxidase activity. Thereafter the slides were pre-incubated with 30 % normal goat serum in PBS for 30 min to reduce non-specific antibody binding. A mouse polyclonal antibody directed against *H. pylori* (DAKO), diluted 1/20 in PBS, was incubated overnight at 21 °C in a moist chamber. The sections were washed and incubated with biotinylated swine anti-rabbit immunoglobulins at 21 °C for 30 min and after rinsing covered with peroxidase conjugated streptavidin-biotin-complex (ABC). Peroxidase activity was developed using H₂O₂ with diaminobenzidine (DAB) as a chromogen (Fast DAB Tablet Set, Sigma-Aldrich). Subsequently, the sections were counterstained with Mayer's hematoxylin and mounted. As a negative control, the primary antibody was replaced with fetal calf serum in Tris-HCl buffer (pH 7.6). As a positive control, a section of a mouse stomach experimentally infected with *Helicobacter pylori* LMG 7539^T was used.

Transmission electronmicroscopy

[0083] For "*Candidatus Helicobacter bovis*", three different pyloric samples were selected for electronmicroscopic evaluation based upon the high presence of *Helicobacter*-like organisms in the corresponding immunostained sections.

[0084] For "*Candidatus Helicobacter suis*", two different antral biopsies were selected for electronmicroscopic evaluation based on the high presence of gastrospirillum-like organisms in the corresponding immunostained slides.

[0085] After dehydration in a graded series of acetone washes, the samples were embedded in Spurr low-viscosity resin. Ultrathin sections were poststained with uranyl acetate and lead citrate and examined with an electronmicroscope (Phillips 201 TEM) at an accelerating voltage of 60 kV.

DNA-extraction

[0086] DNA was isolated from the scrapings of the gastric biopsies and from the reference strains by lysis with guanidinium isothiocyanate and DNA was bound to silica particles according to the method of Boom et al. (1990).

Primers and PCR amplification of 16S rDNA

[0087] Broadrange primers *H33f*, *H61f* and *H1368r* were selected from rRNA superfamily VI (*Helicobacter*, *Campylobacter*, *Arcobacter*, *Wolinella*) specific regions of the 16S rRNA gene (Table 2).

[0088] The use of broad range primer *1492RPL* was suggested by Weissburg et al. (1991). A genus *Helicobacter*-specific primer *H274f* was adapted from primer *274r* described by Dewhirst et al. (1994) (Table 2). Primer combinations *H33f*-*H1368r*, *H274f*-*1492RPL* and *H61f*-*1492RPL* were used to amplify a ~ 1.3-Kb, ~ 1.2-Kb and a ~1.4-Kb fragment of "*Candidatus Helicobacter suis*" respectively.

[0089] PCR reactions were performed in a volume of 50 µl containing 10mM Tris HCl (pH 8.3), 50 mM KCl, 3.5 mM MgCl₂, 200 µM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold (Perkin-Elmer, Roche Molecular Systems) and 25 pmol of both forward and reverse primer (Eurogentec). Reactions were covered with mineral oil and PCR was performed in a Biomed-60 thermocycler under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 50 cycles of 30 s at 94 °C, 45 s at 55 °C and 45 s at 72 °C. Final extension was performed for 5 min at 72 °C. DNA-extractions of *Helicobacter acinonychis* LMG 12684^T and *Helicobacter mustelae* LMG 8776 were used as positive controls.

Analysis of amplified samples

[0090] PCR products were separated on 1 % agarose gels and stained with ethidium bromide.

[0091] DNA-extractions of *H. acinonychis* LMG 12684^T and *H. mustelae* LMG 8776 were used as positive controls.

[0092] In order to determine whether PCR products were derived from *Helicobacter*-like organisms, the desired DNA-bands were cut from the gels, diluted 1/2 in distilled water and sequenced using the *H33f* and *H1368r* 5'-Indocarbocyanin (Cy5) for "*Candidatus Helicobacter bovis*" and respectively *H61f* and *1492RPL* Indocarbocyanin (Cy5) labeled for "*Candidatus Helicobacter suis*". Partial sequences were screened for homologous sequences using the NCBI GEN-INFO @ BLAST Network service (<http://www.ncbi.nlm.nih.gov/BLAST/>) (Altschul et al., 1997).

DNA cloning and sequence analysis for "*Candidatus Helicobacter bovis*"

[0093] PCR amplimers comprising the 16S rDNA-sequences derived from four different stomach samples (R2, R3, R5, R6) were each cloned into plasmid vector pGEM-T (Promega Biotech) according to the manufacturer's instructions and transformed into *Escherichia coli* JM109 using standard procedures. Plasmids were purified using the Easy Prep Plasmid Preparation Kit (Pharmacia Biotech). Sequences were determined by the T7-sequencing system (Pharmacia

Biotech). Two primers flanking the multiple cloning sites (T7, SP6) as well as internal primers *H390f* and *H1053r* were used (Table 2). The sequence derived from the clone of the R2 sample (R2XA) was used as reference sequence. This sequence has been assigned Genbank Accession No. AF127028. Sequence analysis was performed with the PCGene software (Intelligenetics)

[0094] PCR amplicons of three other gastric samples (R13, R27, R28) were sequenced without prior cloning (referred to below as direct sequence analysis).

DNA cloning and sequencing for "*Candidatus Helicobacter suis*"

[0095] PCR amplimers comprising the 16S rDNA-sequences from 2 different stomachs (V2B, V4A) were cloned into plasmid vector pGEM-T (Promega Biotech) according to the manufacturer's instructions and transformed into *Escherichia coli* JM109 using standard procedures. Plasmids were purified using the Easy Prep Plasmid Prep Kit (Pharmacia Biotech). Sequences were determined by the T7-sequencing system (Pharmacia Biotech). Two primers flanking the multiple cloning sites (T7 and SP6) as well as internal primers *H390f* and *H1053r* were used (Table 2). Sequence analysis was performed with the PCGene software (Intelligenetics). A reference sequence was determined based on its high length and was compared to the new sequence and the other derived sequences, to check its integrity (see Figures 4 and 5). The reference sequence V2BXA was assigned Genbank Accession No. AF127028.

[0096] PCR amplicons of three other gastric samples (V5, V14, V19) were sequenced without prior cloning (referred to below as direct sequence analysis).

Phylogenetic analysis for "*Candidatus Helicobacter bovis*"

[0097] Phylogenetic analysis was performed using the GeneCompar 2.0 software package (Applied Maths). Sequences of strains belonging to the epsilon subdivision (Table 3) were retrieved from the EMBL data library and were aligned with reference sequence R2XA. A similarity matrix was constructed from the aligned sequences and was corrected for multiple base changes by the method of Jukes & Cantor (1969). Unknown bases and gaps were not considered in the numerical analysis. A phylogenetic tree was constructed using the neighbour-joining method of Saitou & Nei (1987).

Phylogenetic analysis for "*Candidatus Helicobacter suis*"

[0098] Phylogenetic analysis was performed using the GeneCompar 2.0 software package (Applied Maths). All five "*Candidatus Helicobacter suis*" sequences and the sequences of strains belonging to the same phylogenetic lineage (Table 3) were aligned. Using the neighbour-joining method, a phylogenetic tree and corresponding similarity matrix was constructed. Unknown bases and gaps were not considered in the numerical analysis

"*Candidatus Helicobacter bovis*" specific PCR-assay

[0099] "*Candidatus Helicobacter bovis*" specific oligonucleotides *R574f* and *R832r* (Table 2), were selected from variable rDNA regions of the sequences determined by direct and indirect sequence analysis. These primers comprised a 259 bp 16S rDNA-fragment and were used to develop a specific PCR and an *in situ* hybridisation procedure. Within this fragment an internal "*Candidatus Helicobacter bovis*" specific probe *R628f* (Table 2) was selected for southern blot hybridisation purposes.

[0100] PCR reactions were performed in a volume of 50 µl containing 10 mM Tris HCl (pH 8.3), 50 mM KCl, 2.5 mM MgCl₂, 200 µM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold, and 25 pmol of both forward and reverse primer. PCR amplification was performed under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 40 cycles of 30 s at 94 °C, 45 s at 60 °C and 90 s at 72 °C. Final extension was performed for 5 min at 72 °C. All gastric DNA-extracts were tested with this PCR. For positive controls, plasmid DNA was used from the cloned 16S rDNA fragments (R2XA). As a negative control a DNA-extract was used from an abomasum lacking of *Helicobacter*-like organisms.

[0101] Specificity of the "*Candidatus Helicobacter bovis*" specific oligonucleotides *R574f* and *R832r* was tested by PCR using DNA-extracts of 15 different *Helicobacter* strains and a *Wolinella succinogenes* strain (Table 1).

[0102] PCR products were separated on 2 % agarose gels, stained with ethidium bromide and transferred to Hybond N+ (Amersham) by electro-elution. Southern blot hybridisation was performed with the [³²P] ATP labelled probe *R628f* (Table 2) according to standard procedures (Amersham Pharmacia Biotech). In order to ensure the specificity of the probe hybridisation, blots were washed twice with 0.1 x SSC + 0.1 % SDS at 55°C.

"*Candidatus Helicobacter suis*" specific diagnostic PCR-assay and Southern blot hybridisation

[0103] "*Candidatus Helicobacter suis*"- specific primers (V832f and V1261r) were selected from variable rDNA regions of the sequences determined by direct and indirect sequence analysis, comprising a ~0.4-Kb 16S rDNA-fragment. Within this fragment a "*Candidatus Helicobacter suis*"-specific probe V1000f (Table 2) was selected for hybridisation purposes. PCR reactions were performed in a volume of 50 µl containing 10 mM Tris HCl (pH 8.3), 50 mM KCl, 2.5 mM MgCl₂, 200 µM of each deoxynucleoside triphosphate, 1.5 U of AmpliTaq Gold (Perkin-Elmer), and 25 pmol of both forward and reverse primer (Eurogentec). PCR amplification was performed under the following conditions: 9 min preincubation at 94 °C to activate AmpliTaq Gold, followed by 40 cycles of 30 s at 94 °C, 45 s at 60 °C and 90 s at 72 °C. Final extension was performed for 5 min at 72 °C. As a positive control, plasmid DNA was used from the cloned 16S rDNA fragments (V2B, V4A). As a negative control DNA extracted from the stomach of a gnotobiotic piglet was used.

[0104] To test the specificity of the primers, PCR was also performed on DNA-extracts of 15 different *Helicobacter* species. (Table 1).

[0105] PCR products were separated on 2% agarose gels, stained with ethidium bromide and transferred to Hybond N+ (Amersham) by electro-blotting. Southern blot hybridisation was performed with the [³²P] ATP-labelled probe V1000f according to standard procedures (Amersham Pharmacia Biotech). In order to ensure the specificity of the probe hybridisation, blots were washed twice with 0.1 x SSC + 0.1 % SDS at 55°C.

***In situ* hybridisation for "*Candidatus Helicobacter bovis*"**

[0106] In order to make the link between the "*Candidatus Helicobacter bovis*" specific probe and the bacterial spiral cells observed in the tissue sections, an *in situ* hybridisation procedure was performed on the formalin fixed and paraffin embedded pyloric samples of each animal. A 259-base digoxigenin-labeled probe was synthesized using the "PCR Dig Probe Synthesis Kit" (Boehringer Mannheim) in combination with the "*Candidatus Helicobacter bovis*" specific primers R574f and R832r (Table 2). PCR conditions were identical to those described in the diagnostic PCR assay. The resulting PCR product was purified using the "High Pure PCR Product Purification Kit" (Boehringer Mannheim) following manufacturer's instructions.

[0107] To avoid RNAse activity, all glassware was heated at 180°C for 3 hours. Further precautions included the use of RNAse-free water, and the use of sterile disposable materials whenever possible. Sections of the paraffin-embedded tissues (4 µm thick) were mounted on RNAse-free, APES-coated slides (Sigma-Aldrich) and fixed by heating for 1 hour at 60 °C. The sections were deparaffinized in xylene (2x5 min), rehydrated through graded ethanol, and washed twice in PBS for 5 min each. Sections were then treated with proteinase K (DAKO) for 15 min each at 37 °C in a humidified chamber. The enzyme was inactivated by treatment with 0.2 % glycine in PBS for 3 min. Sections were washed twice in PBS for 5 min each, dehydrated in graded ethanol and air dried. Tissues were circumlined with a DAKO Pen (DAKO) to avoid liquid spillage during further processing and to ensure an efficient sealing of the coverslip. For the hybridisation step, sections were covered with 5 to 15 µl solution, containing 5 ng/µl labeled probe in 50 % deionized formamide, 2x SCC, 10 % dextran sulfate, 0.25 µg/µl yeast t-RNA, 0.5 µg/µl heat denatured salmon sperm DNA, and 1x Denhart's solution. Sections were covered with a piece of coverslip to avoid evaporation. To denature the probe, sections were heated for 10 min at 95 °C and chilled on ice for 10 min. Slides were then hybridised overnight at 37 °C in a humidified chamber. To remove the unbound probe, the coverslips were removed and the sections were washed in 2x SCC and 1x SCC at room temperature for 10 min each followed by two washes of 0.3x SCC at 40 °C for 10 min and at room temperature for 10 min, respectively.

[0108] All steps involving the immunological detection of the hybridised probe were performed at room temperature. The sections were treated first for 30 minutes in Buffer 1 (100mM Tris HCl, 150 mM NaCl, pH 7.5) containing 2 % normal goat serum and 0.3 % Triton X-100. An incubation step followed for 3 hours with diluted (1:30 in the same solution) anti-digoxigenin antibodies conjugated to horse-radish peroxidase (DAKO). Unbound antibodies were washed gently on a shaker with Buffer 1 followed by Buffer 2 (100 mM Tris HCl, 100 mM NaCl, 50 mM MgCl₂, pH 9.5) for 15 min each. To optimize the detection level, the "Tyramid Signal Amplification System" (NEN Life Science Products) was applied on each section, following manufacturer's instructions. The hybridised probe was then visualized, using H₂O₂ with diaminobenzidine as a chromogen (Fast DAB Tablet Set, Sigma-Aldrich). Thereafter the sections were counter-stained with Mayer's hematoxylin and mounted.

***In situ* hybridisation for "*Candidatus Helicobacter suis*"**

[0109] To link the derived sequence to the corresponding organism, an *in situ* hybridisation procedure was performed on the formalin fixed and paraffin embedded pyloric samples of each animal. A ~0.4 Kb digoxigenin-labeled probe was synthesized using the "PCR Dig Probe Synthesis Kit" (Boehringer Mannheim) in combination with the "*Candidatus*

Helicobacter suis-specific primers *V832f* and *V1261r* (Table 2). The rest of the method was performed as mentioned above for "*Candidatus Helicobacter bovis*".

Nucleotide sequence accession numbers

[0110] Accession numbers of the 16S rDNA gene sequences used for the phylogenetic analysis are listed in table 3.

[0111] The 16S rDNA nucleotide sequence of "*Candidatus Helicobacter bovis*" has been deposited in the Genbank database under accession number AF127027.

[0112] The 16S rDNA nucleotide sequence of "*Candidatus Helicobacter suis*" has been deposited in the Genbank database under accession number AF127028.

Results

Urease activity and immunohistochemical evaluation for the cattle samples

[0113] Urease activity was observed in all pyloric samples (7/7). In the fundic samples, urease activity was absent (0/7). Spiral immunostained organisms were observed in the pyloric samples of all animals. The highest concentration was seen in the most distal pyloric samples. They were mostly situated in the mucus layer and in the lumen of the proximal part of the gastric crypts where they formed small clusters. In some samples, coccoid organisms, were observed between the spiral bacteria, which also crossreacted with the *H. pylori* polyclonal antibodies. In the positive control only *Helicobacter pylori* - like bacteria were stained while in the negative controls no staining was observed.

Urease activity and immunohistochemical evaluation for the pig samples

[0114] Tightly coiled immunostained spiral organisms, morphologically similar to "*Gastrospirillum suis*" (Queiroz et al., 1990) were observed in all stomachs (5/5), which was consistent with the presence of urease activity (5/5). The gastrospirillum-like organisms were seen laying separately or in small clusters with a patchy distribution over the sample, and were found mostly in the superficial part of the gastric crypts. Some bacteria revealed bipolar immunostained flagellae. Immunostained coccoid-like organisms were also observed in the pyloric crypts. In the positive control, only *Helicobacter pylori*-like bacteria were stained while in the negative controls no labeling was observed.

Transmission electronmicroscopy for "*Candidatus Helicobacter bovis*"

[0115] Large groups of multiple spiral bacteria were seen within the crypts of the gastric mucosa. There was no obvious cell association between the bacteria and the gastric cells, neither were there any intracellular bacterial inclusions. The bacteria were helical-shaped and had 1-3 complete spiral turns per cell with a wavelength of approximately 750 nm. Cells were 1 - 2.5 µm long and 0.3 µm wide. At least four flagelles were seen at one end. It was unclear whether these flagellae were uni- or bipolar, neither could the presence or absence of a flagella sheath be noted.

Transmission electronmicroscopy for "*Candidatus Helicobacter suis*"

[0116] Within the gastric crypts of the antral region, longitudinal and transversal sections of spiral organisms could be seen. All bacteria had the same characteristic tightly coiled appearance, typical of *Helicobacters* with the gastrospirillum morphology. The length of cells varied from 2.5 to 3.5 µm and they were approximately 0.6 µm wide. Multiple complete spiral turns with a wavelength of ± 600 nm were seen in all longitudinal sections. As only few longitudinal sections of the bacteria were obtained, the number and implantation of the flagellae could not be studied although partial fragments were observed. The bacteria were not seen intracellularly nor was there any obvious cell association with the surrounding epithelial cells. The presence or absence of a flagella sheath could not be noted.

Amplification, cloning and sequencing of *Helicobacter*-like 16S rDNA fragments from cattle samples

[0117] PCR amplification of the 16S rRNA gene using the *H33f* and *H1368r* primers, produced a fragment of the expected size range (± 1.3 Kbp) in all seven samples examined. Partial direct sequence analysis of four of these bands (R2, R3, R5, R6) and subsequent database comparison (BLAST) confirmed the PCR products to be *Helicobacter*-like 16S rDNA fragments. Four PCR products (R2, R3, R5, R6) were cloned followed by partial screening. In one clone a *Clostridium*-like 16S rDNA fragment was found. In all other clones *Helicobacter*-like fragments were inserted. The 16S rDNA sequences of four clones derived from different animals (R2XA, R3XA, R5XE, R6XA), were determined. Additional sequences of three other samples (R13, R27, R28) were characterized by direct sequence analysis using the

primers *H33f*, *H1368r*, *H390f* and *H1053r*.

Amplification, cloning and sequencing of *Helicobacter*-like 16S rDNA fragments from pig samples

- 5 [0118] Several combinations of PCR primers yielded sequences of the expected size. The length of these amplified fragments varied between 1.2 Kb (*H274f-1492RPL*) and 1.4 Kb (*H61f-1492RPL*). The latter primer combination was used to examine all samples. The 16S rDNA sequences of two different clones were determined (V2BXA, V4AXA). Additional sequences of 3 other samples (V5, V14, V19) were determined by direct sequence analysis.

10 Sequences and phylogenetic analysis for cattle samples

- [0119] Sequence length varied from 1267 to 1335 basepairs. Pairwise comparisons between these 7 sequences revealed a sequence homology of more than 99 %. One reference sequence (R2XA) of 1335 bp (see Figure 1: SEQ ID NO 1) was selected for phylogenetic evaluation. A similarity matrix based on comparisons of 16S rRNA sequences of 23 strains representing all validly named *Helicobacter* species, "*Helicobacter heilmannii*" (type1, type2), *Campylobacter jejuni*, *Arcobacter cryaerophilus* and *Wollinella succinogenes* was calculated. By this analysis it was shown that the sequences of the bovine *Helicobacter*-like organisms form a distinct group within the genus *Helicobacter* with *Helicobacter bilis* as closest taxonomic relative (level of similarity 92.8 %). The reference sequence was clearly distinct from sequences belonging to other superfamily VI genera, as shown by a 85.6, 85.1 % and 89.7 % homology with *Campylobacter jejuni*, *Arcobacter butzleri* and *Wollinella succinogenes* respectively. A phylogenetic tree based on this analysis is shown in Fig. 3A.

Sequences and phylogenetic analysis for pig samples

- 25 [0120] The 5 sequences that were determined had lengths varying from 1345 to 1421 basepairs. Pairwise comparisons between 1345 bp consensus fragments of these sequences, revealed a minimum homology of 97.7 %. One reference sequence of 1421 bp, obtained from PCR product 2BXA (see Figure 2: SEQ ID NO 2), was used for phylogenetic analysis. A similarity matrix was calculated based on comparisons of 16S rDNA sequences of all *Helicobacter* species, "*Helicobacter heilmannii*" type 1 and type 2, *Campylobacter jejuni*, *Arcobacter butzleri* and *Wollinella succinogenes* (Table 3). In this analysis, the sequence of the porcine gastrospirillum-like organism formed a distinct subgroup within the *Helicobacter* lineage together with other gastrospirilla: *Helicobacter felis*, *H. bizzozeronii*, *H. salomonis*, "*H. heilmannii*" type 1 and type 2. The sequence was highly similar to that of "*H. heilmannii*" type 1 (level of similarity 99.5 %). The similarity level of other gastrospirillum-like bacteria, *H. felis*, *H. bizzozeronii*, *H. salomonis* and *H. heilmannii* type 2 was 96.4 %, 96.5 %, 96.6 % and 96.8 % respectively. The reference sequence was clearly distinct from sequences belonging to other superfamily VI-genera, as shown by a 86.2 %, 84.7 % and 89.6 % homology with *Campylobacter jejuni*, *Arcobacter butzleri* and *Wollinella succinogenes* respectively.

[0121] A phylogenetic tree based on this analysis is shown in Figure 3B.

Diagnostic PCR-assay for "*Candidatus Helicobacter bovis*"

- 40 [0122] A 259 base fragment was produced for all seven stomach samples with primer pair *R574f-R832r*. All PCR products crosshybridised with the *R628f* probe after southern blot hybridisation. No amplification product was obtained using DNA preparations from any of the *Helicobacter* strains, nor from the bovine *Wollinella succinogenes* strain (Table 1). The positive control yielded a ~0.3 Kb product as expected. There was no DNA-amplification using the negative control material.

"*Candidatus Helicobacter suis*"-specific PCR and Southern blot hybridisation

- 50 [0123] Amplification of *Helicobacter* DNA using the primers *V832f* and *V1261r* produced a 433-base fragment from all five stomach samples. All PCR products hybridised with the *V1000f* probe after Southern blot hybridisation. No amplification product was obtained using DNA preparations from any of the *Helicobacter* strains including *H. felis*, *H. bizzozeronii* and *H. salomonis* (Table 1), nor from the negative control. PCR with the cloned reference material (2BXA) yielded a ~0.4 Kb product as expected.

55 *In situ* hybridisation for "*Candidatus Helicobacter bovis*"

- [0124] *In situ* hybridisation of the bovine *Helicobacter*-like bacteria with the "*Candidatus Helicobacter bovis*"- specific probe was seen in sections from all (7/7) stomachs. These bacteria were observed as darkbrown spiral organisms,

organised in small clusters, situated in the gastric crypts of the pyloric part of the abomasal stomach. Not all spiral bacteria were stained. Sometimes a faint background, seen as fine stained strings, was observed in the surrounding cells. This background staining was also observed in the *H. pylori*-infected mouse stomach which was used as a negative control. The *H. pylori* cells in this control though did not hybridise with the "*Candidatus Helicobacter bovis*"-specific probe.

In situ hybridisation for "*Candidatus Helicobacter suis*"

[0125] *In situ* hybridisation of "*Gastrosprillum suis*"-like bacteria with the "*Candidatus Helicobacter suis*"- specific probe was seen in sections from all (5/5) stomachs. Bacteria were observed as darkbrown spiral organisms in the superficial mucus layer and the gastric crypts. In some cases, helical organisms located deeply in the crypts, were weakly labeled or were negative. Sometimes a faint background, seen as fine stained strings, was observed in the surrounding cells. This background staining was also observed in the *H. pylori*-infected mouse stomach which was used as a negative control. The *H. pylori* cells in this control though did not hybridise with the "*Candidatus Helicobacter suis*"- specific probe.

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Table 1:

Bacterial strains used for the evaluation of the " <i>Candidatus Helicobacter bovis</i> " specific PCR		
Taxon	Source	Collection N° or Strain
<i>Helicobacter acinonychis</i>	Cheetah gastric mucosa	LMG 12684 ^T
<i>Helicobacter cinaedi</i>	Human feces	LMG 7543 ^T
<i>Helicobacter</i> sp. strain CLO-3	Human rectal swab	LMG 7792
<i>Helicobacter fennelliae</i>	Human feces	LMG 11759
<i>Helicobacter pametensis</i>	Tern feces	LMG 12678 ^T
<i>Helicobacter</i> sp. strain Bird B	Bird feces	LMG 12679
<i>Helicobacter</i> sp. strain Bird C	Bird feces	LMG 13642
<i>Helicobacter hepaticus</i>	Murine liver	LMG 16316 ^T
<i>Helicobacter pullorum</i>	Chicken lower bowel	LMG 16318
<i>Helicobacter mustelae</i>	Ferret gastric mucosa	LMG 18044 ^T
<i>Helicobacter canis</i>	Canine feces	LMG 18086 ^T
<i>Helicobacter muridarum</i>	Murine intestinal mucosa	LMG 14378 ^T
<i>Helicobacter bizzozeronii</i>	Canine gastric mucosa	Strain 12A
<i>Helicobacter saloonionis</i>	Canine gastric mucosa	CCUG 37845 T
<i>Helicobacter felis</i>	Feline gastric mucosa	CCUG 28539 T

Table 2: Oligonucleotide primers and probe used for PCR amplification, sequencing of genes coding for 16S rRNA and Southern blot hybridisation

Primers	Sequences (5'-3')	<i>Escherichia coli</i> 16S rRNA position
<i>H33f</i>	ACG CTG GCG GCG TGC CTA ATA CAT GCA AGT CG	33-64 (SEQ ID NO 3)
<i>H1368r</i>	GGT GAG TAC AAG ACC CGG GAA CGT ATT CAC CG	1368-1388 (SEQ ID NO 4)
<i>H390f</i>	GCA GCA ACG CCG CGT GGA GGA TGA	390-413 (SEQ ID NO 5)
<i>H1053r</i>	ACG AGC TGA CGA CAG CCG TG	1053-1072 (SEQ ID NO 6)
<i>R574f</i>	AGA GCG TGT AGG CGG AAT GAT	574-593 (SEQ ID NO 7)
<i>R628f</i>	AAC TGC GTT TGA AAC TAT CAT T	628-649 (SEQ ID NO 8)
<i>H61f</i>	TGC AAG TCG AAC GAT GAA GC	61-76 (SEQ ID NO 9)
<i>H274f</i>	AGG CTA TGA CGG GTA TCC GGC CTG AGA	274-299 (SEQ ID NO 10)
<i>I492RPL</i>	GCC GCC CGG GTT ACC TTG TTA CGA CTT	832-852 (SEQ ID NO 11)
<i>V832f</i>	TTG GGA GGC TTT GTC TTT CCA	1000-1020 (SEQ ID NO 12)
<i>V1261r</i>	GAT TAG CTC TGC CTC GCG GCT	1261-1281 (SEQ ID NO 13)

V1000f AGG AAT TCC CTA GAA ATA GGG 1000-1020 (SEQ ID
 NO 26)

R832r CGA GGA GAC AAG CCC CCC GA 832-851 (SEQ ID
 NO 14)

Table 3:

Sources and accession numbers of strains used for phylogenetic analysis.		
Taxon	Source	Genbank Accession N°
" <i>Gastrosipillum hominis</i> " type 1	Human gastric mucosa	L10079
" <i>Gastrosipillum hominis</i> " type 2	Human gastric mucosa	L10080
<i>Helicobacter acinonychis</i>	Cheetahgastric mucosa	M88148
<i>Helicobacter bilis</i>	Murine liver	U18766
<i>Helicobacter bizzozeronii</i>	Canine gastric mucosa	Y09404
<i>Helicobacter canis</i>	Canine feces	L13464
<i>Helicobacter cholecystus</i>	Murine liver	U46129
<i>Helicobacter cinaedi</i>	Human feces	M88150
<i>Helicobacter felis</i>	Feline gastric mucosa	M57398
<i>Helicobacter fennelliae</i>	Human feces	M88154
<i>Helicobacter hepaticus</i>	Murine liver	U07574
<i>Helicobacter muridarum</i>	Murine intestinal mucosa	M80205
<i>Helicobacter mustelae</i>	Ferret gastric mucosa	M35048
<i>Helicobacter nemestrinae</i>	Macaque gastric mucosa	X67854
<i>Helicobacter pametensis</i>	Swine feces	M88155
<i>Helicobacter pullorum</i>	Broiler chicken cecum	L36141
<i>Helicobacter pylori</i>	Human gastric mucosa	M88157
<i>Helicobacter salomonis</i>	Canine gastric mucosa	Y09405
<i>Helicobacter trogonum</i>	Rat colon mucosa	U65103
<i>Helicobacter rodentium</i>	Murine intestinal mucosa	U96297
<i>Arcobacter butzleri</i>	Human	L14626
<i>Campylobacter jejuni</i>	Human feces	L14630
<i>Wolinella succinogenes</i>	Cattle abomasal mucosa	M88159

Annex to the application documents - subsequently filed sequences listing

[0185]

5

SEQUENCE LISTING

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<120> New gastric Helicobacter 16 S rDNA sequences from
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 <212> DNA
 <213> Helicobacter sp.

10 <400> 15
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 <213> Helicobacter sp.

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55

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10 <210> 17
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 <212> DNA
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35 <210> 18
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 <212> DNA
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5 tcggctgggc actctaagga gactgccttc gtaaggagga ggaaggcgag gatgacgtca 1080
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<210> 19

<211> 1194

<212> DNA

<213> *Helicobacter* sp.

<400> 19

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 aactcaaaaa catctcccag ttcggattgt ggtctgcaac tcgaccacat gaag 1194

<210> 20

<211> 1172

<212> DNA

<213> *Helicobacter* sp.

<400> 20

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 ggggaaaccc tgaagcagca acgcccgtg gaggatgaag gttctaggat tgtaaactcc 300
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1172

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<210> 21

<211> 1400

<212> DNA

<213> Helicobacter sp.

10

<400> 21

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<210> 22

<211> 1353

<212> DNA

<213> Helicobacter sp.

<400> 22

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 <212> DNA
 <213> *Helicobacter* sp.

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<210> 24
 <211> 1358
 <212> DNA
 40 <213> *Helicobacter* sp.

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 <210> 25
 15 <211> 21
 <212> DNA
 <213> *Helicobacter* sp.

 <400> 25
 20 aggaattccc tagaaatagg g 21

25

Claims

1. An isolated 16S rDNA *Helicobacter* polynucleic acid sequence selected from any of the following
 - 30 (a) a sequence represented in any of SEQ ID NO 1 to 2, or, the 16S rRNA sequence encoded thereby,
 - (b) a sequence which hybridizes under stringent conditions to any of the sequences defined in (a).
2. An isolated polynucleic acid sequence according to claim 1 represented by any of SEQ ID NO 1 to 2 or 15 to 24.
3. An isolated polynucleic acid sequence according to claim 1 which is more than 92.8%, preferably more than 93.5%, more preferably more than 95% and most preferably more than 97.5% homologous to SEQ ID NO 1.
4. A part of an isolated polynucleic acid according to any of claims 1 to 3, wherein said part is unique to the polynucleic acid sequence it is derived from.
5. A probe which specifically hybridizes to a polynucleic acid sequence according to any of claims 1 to 4.
6. A primer which specifically amplifies a polynucleic acid sequence according to any of claims 1 to 4.
7. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising hybridizing the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one probe according to claim 5.
8. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically amplifying the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one primer according to claim 6.
9. A method for detection and/or typing of *Helicobacter* strains present in a biological sample comprising specifically hybridizing or specifically amplifying the 16S rRNA gene target region polynucleotides of said *Helicobacter* strains present in said biological sample with at least one sequence which is more than 96.6% homologous to SEQ ID NO 2, or a sequence specific primer or a sequence specific probe derived thereof.

10. A diagnostic kit for detection and/or typing of *Helicobacter* strains comprising:

- at least one probe according to claim 5 or 9, and/or,

5 - at least one primer according to claim 6 or 9.

11. A medicament comprising a polynucleic acid sequence according to any of claims 1 to 6.

12. A polynucleic acid sequence according to any of claims 1 to 6 for use as a medicament.

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          *           20           *
HbovisR2XA : -----ACGCT : 5
Hpylori|gb : TTTATGGAG-----CAGAGTGAACGCT : 37
Hbilis|gb| : -----CAGAGTGAACGCT : 28
Hcanis|gb| : -----CAGAGTGAACGCT : 28
Hcinaedi|g : -TTATGGAG-----CAGAGTGAACGCT : 36
Hacinonych : TTTATGGAG-----CAGAGTGAACGCT : 37
Hnemestrin : NNTATGGAG-----CAGAGTGAACGCT : 37
Hcholescys : -----CAGAGTGAACGCT : 18
Hpamatsensi : -TTATGGAG-----CAGAGTGAACGCT : 36
Hmustelae| : ATTATGGAG-----CAGAGTGAACGCT : 37
Hrodentium : -----CAGAGTGAACGCT : 14
Hpullorum| : -----G-----CAGAGTGAACGCT : 29
Hfennellia : TTTACGGAG-----CAGAGTGAACGCT : 37
Htrogonum : -----CAGAGTGAACGCT : 14
Hmuridarum : ---ATGGAG-----CAGAGTGAACGCT : 34
Hhepaticus : -----CAGAGTGAACGCT : 13
Ghominis1| : -----AGTGAACGCT : 10
Ghominis2| : -----AGTGAACGCT : 10
Hfelis|gb| : TTTATGGAG-----CAGAGTGAACGCT : 37
Hbizzozero : -----AGTGAACGCT : 10
Hsalomonis : ----- : -
Abutzleri| : ---ATGGAG-----CAGAGTGAACGCT : 34
Cjejuni|gb : --TATGGAG-----CAGAGTGAACGCT : 35
Wsuccinoge : -TTATGGAG-----CAGAGTGAACGCT : 36
                                cagagtgaacgct

```

Figure 1 - 1

	40	*	60	*	
HbovisR2XA :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAA	:	42		
Hpylori gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	74		
Hbilis gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	65		
Hcanis gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	65		
Hcinaedi g :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	73		
Hacinonych :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	74		
Hnemestrin :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAA	:	74		
Hcholescys :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	55		
Hpamatensi :	GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG	:	73		
Hmustelae :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	74		
Hrodentium :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	51		
Hpullorum :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	66		
Hfennellia :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	74		
Htrogontum :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	51		
Hmuridarum :	GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG	:	71		
Hhepaticus :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAT	:	50		
Ghominis1 :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	47		
Ghominis2 :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	47		
Hfelis gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	74		
Hbizzozero :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG	:	47		
Hsalomonis :	-----GAAG	:	4		
Abutzleri :	GGCGGCGTGCCTAATACATGCAAGTCGAACGAGAAACG	:	71		
Cjejuni gb :	GGCGGCGTGCCTAATACATGCAAGTCGNACGATGAAG	:	72		
Wsuccinoge :	GGCGGCGTGCCTAATACATGCAAGTCGAACGGTAAACA	:	73		
	ggcggcgtgcctaatacatgcaagtcgaacgatgAag				

Figure 1 - 2

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      80          *          100          *
HbovisR2XA : TT C-TAGCTTGCTAGGAATG---GATTAGTGGCGCA : 75
Hpylori|gb : CT C-TAGCTTGCTAGAGTGCT--GATTAGTGGCGCA : 108
Hbilis|gb| : CT C-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 98
Hcanis|gb| : CT T-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 98
Hcinaedi|g : CT T-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 106
Hacinonych : CT C-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 107
Hnemestrin : CTCT-AAGCTTGC---ATGCT--GATTAGTGGCGCA : 104
Hcholescys : CT T-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 88
Hpamatensi : CTCTCTAGCTTGCTAGAGTG--GATTAGTGGCGCA : 108
Hmustelae| : CT C-TAGCTTGCTAGAGTG--GATTAGTGGCGCA : 107
Hrodentium : C--TC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 82
Hpullorum| : C--TC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 99
Hfennellia : TC C-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 107
Htrogonum : CT T-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 84
Hmuridarum : CT T-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 104
Hhepaticus : CT C-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 83
Ghominis1| : C--C-TAGCTTGCTAG---TT--GATTAGTGGCGCA : 75
Ghominis2| : C--C-TAGCTTGCTAG---GTG--GATTAGTGGCGCA : 76
Hfelis|gb| : C--C-TAGCTTGCTAG---GCG--GATTAGTGGCGCA : 103
Hbizzozero : C--C-TAGCTTGCTAG---GTG--GATTAGTGGCGCA : 76
Hsalomonis : C--C-TAGCTTGCTAG---GCG--GATTAGTGGCGCA : 33
Abutzleri| : GATTATAGCTTGCTATATTGTCAAGCTAAGTGGCGCA : 108
Cjejuni|gb : C--TC-TAGCTTGCTAGAGTG---GATTAGTGGCGCA : 105
Wsuccinoge : GGGTGTAGCTTGCTATCTGCT--GACGAGTGGCGCA : 108
      c      tAGCTTGctag      gattAGTGGCGCA

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Figure 1 _ 3

	120	*	140	
HbovisR2XA :	CGGGTGAGTAA	GCATAG	-AA	TGCCC
Hpylori gb :	CGGGTGAGTAA	GCATAG	TC	TGCCC
Hbilis gb :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hcanis gb :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hcinaedi g :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hacinonych :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hnemestrin :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hcholescys :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hpamatensi :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hmustelae :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hrodentium :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hpullorum :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hfennellia :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Htrogontum :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hmuridarum :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hhepaticus :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Ghominis1 :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Ghominis2 :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hfelis gb :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hbizzozero :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Hsalomonis :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Abutzleri :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Cjejuni gb :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
Wsuccinoge :	CGGGTGAGTAA	GCATAG	TTA	TGCCC
	CGGGTGAGTAA	GcATAG	t A	TGCCc ttAgt t

Figure 1 - 4

	*	160	*	180	
HbavisR2XA :	GGG	ATAGCCA	CGG	AAACAGT	GATTAAATACTAATAC : 148
Hpylori gb :	GGG	ATAGCCA	TGG	AAACGAT	GATTAAATACCAATAC : 182
Hbilis gb :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATCTGATAC : 172
Hcanis gb :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATCTGATAC : 172
Hcinaedi g :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATCTGATAC : 180
Hacinonych :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATACCAATAT : 181
Hnemestrin :	GGG	ATAGCCA	TGG	AAACGAT	AGATAATACCAATAC : 178
Hcholescys :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATACCGATAC : 162
Hpamatensi :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATACCAATAC : 182
Hmustelae :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATCTGATAC : 181
Hrodentium :	AGG	ATAGCCA	TGG	AAACGAT	GATTAAATCTGATAC : 156
Hpullorum :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATACCAATAC : 173
Hfennellia :	AGG	ATANNNN	NNG	AAACGGT	GATTAAATACNNNNNN : 181
Htrogontum :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATACCGATAC : 158
Hmuridarum :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATCTGATAC : 178
Hhepaticus :	GGG	ATAGCCA	TGG	AAACGGT	GATTAAATCTGATAC : 157
Ghominis1 :	GGA	ATAGCCA	TAG	AAATGGT	GATTAAATACCAATAC : 149
Ghominis2 :	GGG	ATAGCCA	TAG	AAATGGT	GATTAAATACCAATAT : 150
Hfelis gb :	GGG	ATAGCCA	TAG	AAATGGT	GATTAAATACCAATAC : 177
Hbizzozero :	GGG	ATAGCCA	TAG	AAATGGT	GATTAAATACCAATAC : 150
Hsalomonis :	GGG	ATAGCCA	TAG	AAATGGT	GATTAAATACCAATAC : 107
Abutzleri :	GGG	ATAGCCA	TGG	AAACGAT	TGCTAATACCTTATAT : 182
Cjejunigb :	AGG	ATAGCCA	TGG	AAACGAT	TGCTAATACCTTATAC : 179
Wsuccinoge :	GGA	ATAGCCA	TGG	AAACGGT	GATTAAATACCGATAT : 182
	gGg	AtAgCca	tgG	AAAcggtgatt	TAATAC ATAc

Figure 1 5

	*	200	*	220	
HbovisR2XA :	GC	CT	-----	AAGGGGGAAAGA	--ATT : 169
Hpylori gb :	T	CT	-----	AAGGGGCAAGAGA	--TTT : 201
Hbilis gb :	TC	CT	-----	AAGGGGCAAGGGGCTTT	: 195
Hcanis gb :	TC	CT	-----	ATGGGGCAAG	---TTT : 191
Hcinaedi g :	TC	T	-----	AAGGGGCAAGG	---TTT : 199
Hacinonych :	T	CT	-----	AAGGGGCAAGAGA	---TTT : 200
Hnemestrin :	T	CT	-----	AAGGGGCAAGAGA	---TTT : 197
Hcholescys :	T	CCC	-----	TACGGGGCAAG	---TTT : 181
Hpamatensi :	T	CT	-----	TACGAGGCAAG	---TTT : 201
Hmustelae :	T	CT	-----	AAGGGGCAAG	---NTN : 200
Hrodentium :	TC	CT	-----	AAGGGGCAAG	---TTT : 175
Hpullorum :	TC	CT	-----	AAGGGGCAAG	---TTT : 192
Hfennellia :	N	---RNN	-----	NNNNNNNNNNNN	---NNC : 200
Htrogontum :	TC	TT	-----	AGGAGGCAAG	---TTT : 177
Hmuridarum :	TC	---	T-----	AAGGGGCAAG	---TTT : 196
Hhepaticus :	TC	CT	-----	AAGGGGCAAG	---TTT : 176
Ghominis1 :	TA	CTT	-----	AAGGCAAGAGA	---TTT : 170
Ghominis2 :	TA	CCCT	---7---	AAGGGGCAAGAGA	---TTT : 171
Hfelis gb :	T	CT	-----	AAGGGGCAAGAGA	---TTT : 196
Hbizzozero :	TA	CCCT	-----	ATGGGGCAAGAGA	---TTT : 171
Hsalomonis :	TA	CCCT	-----	ATGGGGCAAGAGA	---TTT : 128
Abutzleri :	TC	TTTTTATCAAAAGATA	AAAAGGGGCAAGAGA	---TTT : 216	
Cjejuni gb :	TC	TGCTTAACACAAGTTG	GTAGGGCAAG	---TNT : 212	
Wsuccinoge :	TC	CG	-----	AGAGGGGCAAG	---TTT : 201
	t	c		a gggGGaAAg	TTt

Figure 1 - 6

	*	240	*	26	
HbovisR2XA :	-----				-
Hpylori gb :	-----				-
Hbilis gb :	CAATAAAGAATTTCTCTTTT		AGTGCTTTGTGTTGTT		232
Hcanis gb :	-----				-
Hcinaedi g :	-----				-
Hacinonych :	-----				-
Hnemestrin :	-----				-
Hcholescys :	-----				-
Hpamatensi :	-----				-
Hmustelae :	-----				-
Hrodentium :	-----				-
Hpullorum :	-----				-
Hfennellia :	-----				-
Htrogontum :	-----				-
Hmuridarum :	-----				-
Hhepaticus :	-----				-
Ghominis1 :	-----				-
Ghominis2 :	-----				-
Hfelis gb :	-----				-
Hbizzozero :	-----				-
Hsalomonis :	-----				-
Abutzleri :	-----				-
Cjejuni gb :	-----				-
Wsuccinoge :	-----				-

Figure 1 - 7

	0	*	280	*	
HbovisR2XA :	-----				-
Hpylori gb :	-----				-
Hbilis gb :	GGCACAAAATTCTAGTATTTGGAATGAGAAATTGATG				269
Hcanis gb :	-----				-
Hcinaedi g :	-----				-
Hacinonych :	-----				-
Hnemestrin :	-----				-
Hcholescys :	-----				-
Hpamatensi :	-----				-
Hmustelae :	-----				-
Hrodentium :	-----				-
Hpullorum :	-----				-
Hfennellia :	-----				-
Htrogontum :	-----				-
Hmuridarum :	-----				-
Hhepaticus :	-----				-
Ghominis1 :	-----				-
Ghominis2 :	-----				-
Hfelis gb :	-----				-
Hbizzozero :	-----				-
Hsalomonis :	-----				-
Abutzleri :	-----				-
Cjejuni gb :	-----				-
Wsuccinoge :	-----				-

Figure 1 - 8

	300	*	320	*	
HbovisR2XA :	-----		-----		-
Hpylori gb :	-----		-----		-
Hbilis gb :	TTGTGAAGCAATTTGTGCGGAGACTAGACTTAGTGTC				306
Hcanis gb :	-----		-----		-
Hcinaedi g :	-----		-----		-
Hacinonych :	-----		-----		-
Hnemestrin :	-----		-----		-
Hcholescys :	-----		-----		-
Hpamatensi :	-----		-----		-
Hmustelae :	-----		-----		-
Hrodentium :	-----		-----		-
Hpullorum :	-----		-----		-
Hfennellia :	-----		-----		-
Htrogontum :	-----		-----		-
Hmuridarum :	-----		-----		-
Hhepaticus :	-----		-----		-
Ghominis1 :	-----		-----		-
Ghominis2 :	-----		-----		-
Hfelis gb :	-----		-----		-
Hbizzozero :	-----		-----		-
Hsalomonis :	-----		-----		-
Abutzleri :	-----		-----		-
Cjejuni gb :	-----		-----		-
Wsuccinoge :	-----		-----		-

Figure 1 - 9

	340	*	360	*	
HbovisR2XA :	-----		-----		-
Hpylori gb :	-----		-----		-
Hbilis gb :	TGTCGCACAAGCAAATTGCGAACTCATCGATTTATCG				343
Hcanis gb :	-----		-----		-
Hcinaedi g :	-----		-----		-
Hacinonych :	-----		-----		-
Hnemestrin :	-----		-----		-
Hcholescys :	-----		-----		-
Hpamatensi :	-----		-----		-
Hmustelae :	-----		-----		-
Hrodentium :	-----		-----		-
Hpullorum :	-----		-----		-
Hfennellia :	-----		-----		-
Htrogontum :	-----		-----		-
Hmuridarum :	-----		-----		-
Hhepaticus :	-----		-----		-
Ghominis1 :	-----		-----		-
Ghominis2 :	-----		-----		-
Hfelis gb :	-----		-----		-
Hbizzozero :	-----		-----		-
Hsalomonis :	-----		-----		-
Abutzleri :	-----		-----		-
Cjejuni gb :	-----		-----		-
Wsuccinoge :	-----		-----		-

Figure 1 - 10

	380	*	400	
HbovisR2XA :	-----		CGCTA	: 176
Hpylori gb :	-----	AT	CGCTA G	: 210
Hbilis gb :	TCCAAAGACGAATTTT	ATTGAAAGCCTT	CGCTA	: 380
Hcanis gb :	-----	T	CGCTA	: 200
Hcinaedi g :	-----	T	CGCTA	: 208
Hacinonych :	-----	AT	CGCTA G	: 209
Hnemestrin :	-----	AT	CGCTA G	: 206
Hcholescys :	-----	TT	CGCTA	: 190
Hpamatensi :	-----	TT	CGCTATG	: 210
Hmustelae :	-----	TT	CGCTATG	: 209
Hrodentium :	-----	TT	CGCTA	: 184
Hpullorum :	-----	TT	CGCTA G	: 201
Hfennellia :	-----	TC	CGCTA	: 209
Htrogontum :	-----	TT	CGCTATG	: 186
Hmuridarum :	-----	TE	CGCTA	: 205
Hhepaticus :	-----	TE	CGCTA	: 185
Ghominis1 :	-----	AT	CGCTA	: 179
Ghominis2 :	-----	AT	CGCTA	: 180
Hfelis gb :	-----	AT	CGCTA	: 205
Hbizzozero :	-----	AT	CGCTA	: 180
Hsalomonis :	-----	AT	CGCTA	: 137
Abutzleri :	-----	NT	TGGTA G	: 225
Cjejuni gb :	-----	TT	CGGTGT	: 221
Wsuccinoge :	-----	TT	CGCTATG	: 210
		t	cGcTa	

Figure 1 - II

	*	420	*	440	
HbovisR2XA :	GGAT	AGCTATGTCCTATCAGCT	AGTTGGTGAGGTA	:	213
Hpylori gb :	ACAT	AGCTATGTCCTATCAGCTTGGTGGTA	AAGGTA	:	247
Hbilis gb :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	417	
Hcanis gb :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	237	
Hcinaedilg :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	245	
Hacinonych :	ACAT	AGCTATGTCCTATCAGCTTGGTGGTA	AAGGTA	:	246
Hnemestrin :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTA	AAGGTA	:	243
Hcholescys :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	227	
Hpamatensi :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	247	
Hmustelae :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	246	
Hrodentium :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	221	
Hpullorum :	GGAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	238	
Hfennellia :	GGAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	246	
Htrogontum :	GGAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	223	
Hmuridarum :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	242	
Hhepaticus :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	222	
Ghominis1 :	GGAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	216	
Ghominis2 :	GGAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	217	
Hfelis gb :	GCAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	242	
Hbizzozero :	GCAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	217	
Hsalomonis :	GCAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	174	
Abutzleri :	AGAT	TGGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	262	
Cjejuni gb :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	258	
Wsuccinoge :	GGAT	AGCTATGTCCTATCAGCTTGGTGGTGAGGTA	:	247	
	gGAT	GCTaTgtccTATCAGcTtGTTGGTgaGGTA			

Figure 1 - 12

	*	460	*	480	
HbovisR2XA :	AATGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	250	
Hpylori gb :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	284	
Hbilis gb :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	454	
Hcanis gb :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	274	
Hcinaedi g :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	282	
Hacinonych :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	283	
Hnemestrin :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	280	
Hcholescys :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	264	
Hpamatensi :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	284	
Hmustelae :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	283	
Hrodentium :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	258	
Hpullorum :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	275	
Hfennellia :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	283	
Htrogontum :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	260	
Hmuridarum :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	279	
Hhepaticus :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	259	
Ghominis1 :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	253	
Ghominis2 :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	254	
Hfelis gb :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	279	
Hbizzozero :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	254	
Hsalomonis :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	211	
Abutzleri :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	299	
Cjejuni gb :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	295	
Wsuccinoge :	AAGGCTT	ACCAAGGCTATGACGGGTATCCGGCCTGAG	:	284	

A gGCT ACCAAGGCTATGACGGGTATCCGGCCTGAG

Figure 1 - 13

	*	500	*	5	
HbovisR2XA :	AGGGTGA	CGGACACAC	CGGAAC	TGAGACACGGTCCG	: 287
Hpylori gb :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 321
Hbilis gb :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 491
Hcanis gb :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 311
Hcinaedi g :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 319
Hacinonych :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 320
Hnemestrin :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 317
Hcholescys :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 301
Hpamatensi :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 321
Hmustelae :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 320
Hrodentium :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 295
Hpullorum :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 312
Hfennellia :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 320
Htrogontum :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 297
Hmuridarum :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 316
Hhepaticus :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 296
Ghominis1 :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 290
Ghominis2 :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 291
Hfelis gb :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 316
Hbizzozero :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 291
Hsalomonis :	AGGGTGA	CGGACACACT	CGAAC	TGAGACACGGTCCA	: 248
Abutzleri :	AGGATGA	TCAGTCACACT	TGGAAC	TGAGACACGGTCCA	: 336
Cjejuni gb :	AGCATCA	TCAGTCACACT	TGGAAC	TGAGACACGGTCCA	: 332
Wsuccinoge :	AGGGTGA	CGGACACACT	TGGAAC	TGAGACACGGTCCA	: 321
	AGGgTGA	CgGaCACACT	tGGAAC	TGAGACACGGTCCA	

Figure 1 - 14

	20	*	540	*	
HbovisR2XA :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	324		
Hpylori gb :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	358		
Hbilis gb :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	528		
Hcanis gb :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	348		
Hcinaedi g :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	356		
Hacinonych :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	357		
Hnemestrin :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	354		
Hcholescys :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	338		
Hpamatensi :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	358		
Hmustelae :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	357		
Hrodentium :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	332		
Hpullorum :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	349		
Hfennellia :	GNCTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	357		
Htrogontum :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	334		
Hmuridarum :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	353		
Hhepaticus :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	333		
Ghominis1 :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	327		
Ghominis2 :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	328		
Hfelis gb :	GACTCCNCGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	353		
Hbizzozero :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	328		
Hsalomonis :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	285		
Abutzleri :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	373		
Cjejuni gb :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	369		
Wsuccinoge :	GACTCCTACGGGAGGCAGCAGTAGGGGAATATTGCTCA	:	358		

Figure 1 - 15

	560	*	580	*	
HbovisR2XA :	ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	361	
Hpylori gb :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	395	
Hbilis gb :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	565	
Hcanis gb :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	385	
Hcinaedi g :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	393	
Hacinonych :	ATGGGSGCAAS	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	394	
Hnemestrin :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	391	
Hcholescys :	ATGGGCGAAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	375	
Hpamatensi :	ATGGGCGAAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	395	
Hmustelael :	ATGGGCGAAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	394	
Hrodentium :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	369	
Hpullorum :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	386	
Hfennellia :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	394	
Htrogontum :	ATGGGCGAAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	371	
Hmuridarum :	ATGGGCGAAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	390	
Hhepaticus :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	370	
Ghominis1 :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	364	
Ghominis2 :	ATGGGCGCAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	365	
Hfelis gb :	ATGGGCGCAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	390	
Hbizzozero :	ATGGGCGCAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	365	
Hsalomonis :	ATGGGCGCAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	322	
Abutzleri :	ATGGACGAAAG	TCTGATGCAGCAACGCCGCGTGGAGG	:	410	
Cjejuni gb :	ATGGGGGAAAC	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	406	
Wsuccinoge :	ATGGGCGAAAG	CCCTGAAGCAGCAACGCCGCGTGGAGG	:	395	
	ATGGG	GaAA ccTGAaGCAGCAACGCCGCGTGGAGG			

Figure 1 - 16

	600	*	620	
HbovisR2XA :	ATGAAGGTTCTAGGATTGTAAACTCCTTTTCTGAGAG			: 398
Hpylori gb :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTAGAG			: 432
Hbilis gb :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTAAGAG			: 602
Hcanis gb :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTAAGAG			: 422
Hcinaedi g :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTAAGAG			: 430
Hacinonych :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTCAGAG			: 431
Hnemestrin :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTCAGAG			: 428
Hcholescys :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTGAGAG			: 412
Hpamatensi :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTTAGAG			: 432
Hmustelae :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTAAGAG			: 431
Hrodentium :	ATGAAGGTTTTCGGATTGTAAACTCCTTTTCTAAGAG			: 406
Hpullorum :	ATGAAGGTTTTCGGATTGTAAACTCCTTTTCTTAGAG			: 423
Hfennellia :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTTAGAG			: 431
Htrogontum :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTAAGAG			: 408
Hmuridarum :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTGAGAG			: 427
Hhepaticus :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTTAGAG			: 407
Ghominis1 :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTTAGAG			: 401
Ghominis2 :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTGAGAG			: 402
Hfelis gb :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTCAGAG			: 427
Hbizzozero :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTCAGAG			: 402
Hsalomonis :	ATGAAGGTTTTAGGATTGTAAACTCCTTTTCTGAGAG			: 359
Abutzleri :	ATGACACATTTTCGGTGCCTAAACTCCTTTTCTATATAAG			: 447
Cjejuni gb :	ATGACACATTTTCGGAGCCTAAACTCCTTTTCTTAGGG			: 443
Wsuccinoge :	ATGAAGGTTTTCGGATTGTAAACTCCTTTTCTAAGAG			: 432
	ATGAaggtttTaGGattGTAAACTCCTTTT		T agaG	

Figure 1 - 17

	*	640	*	660	
HbovisR2XA :	AAGA-	TAATGACGGTATCTCAG	GAATAAGCACCGGCT	:	434
Hpylori gb :	AAGA-	TAATGACGGTATCTAAG	GAATAGGACCGGCT	:	468
Hbilis gb :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	638
Hcanis gb :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	458
Hcinaedi g :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	466
Hacinonych :	AAGA-	TAATGACGGTATCTGAG	GAATAAGCACCGGCT	:	467
Hnemestrin :	AAGA-	TAATGACGGTATCTAAG	GAATAAGCACCGGCT	:	464
Hcholescys :	AAGA-	TTATGACGGTATCTCA	GAATAAGCACCGGCT	:	448
Hpamatensi :	AAGA-	TTATGACGGTATCTAAG	GAATAAGCACCGGCT	:	468
Hmustelae :	AAGA-	TAATGACGGTATCTTAG	GAATAAGCACCGGCT	:	467
Hrodentium :	AAGA-	TTATGACGGTATCTTAG	GAATAAGCACCGGCT	:	442
Hpullorum :	AAGA-	TAATGACGGTATCTAAG	GAATAAGCACCGGCT	:	459
Hfennellia :	AAGA-	TTATGACGGTATCTAAG	GAATAAGCACCGGCT	:	467
Htrogontum :	AAGA-	TTATGACGGTATCTTAG	GAATAAGCACCGGCT	:	444
Hmuridarum :	AAGA-	TTATGACGGTATCTCA	GAATAAGCACCGGCT	:	463
Hhepaticus :	AAGA-	TTATGACGGTATCTAAG	GAATAAGCACCGGCT	:	443
Ghominis1 :	AAGA-	TAATGACGGTATCTAAG	GAATAAGCACCGGCT	:	437
Ghominis2 :	AAGA-	TAATGACGGTATCTCA	GAATAAGCACCGGCT	:	438
Hfelis gb :	AAGA-	TAATGACGGTATCTGAG	GAATAAGCACCGGCT	:	463
Hbizzozero :	AAGA-	TAATGACGGTATCTGAG	GAATAAGCACCGGCT	:	437
Hsalomonis :	AAGA-	TAATGACGGTATCTCA	GAATAAGCACCGGCT	:	395
Abutzleri :	AAGA-	TAATGACGGTATCTAAG	GAATAAGCACCGGCT	:	483
Cjejuni gb :	AAGA-	TTATGACGGTATCTAAG	GAATAAGCACCGGCT	:	480
Wsuccinoge :	AAGA-	TTATGACGGTATCTTAG	GAATAAGCACCGGCT	:	468
		AAGA T aTGACGGTAtct A GAaTAAGCACCGGCT			

Figure 1 - 18

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	*	680	*	700	
HbovisR2XA :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 471
Hpylori gb :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 505
Hbilis gb :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 675
Hcanis gb :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 495
Hcinaedi g :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 503
Hacinonych :	NACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 504
Hnemestrin :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 501
Hcholescys :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 485
Hpamatensi :	NACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 505
Hmustelae :	NACTCCGTGCCAGCAGCCGCGGNANTACGGAGGGTGC				: 504
Hrodentium :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 479
Hpullorum :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 496
Hfennellia :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 504
Htrogontum :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 481
Hmuridarum :	NACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 500
Hhepaticus :	AACTCCGTGCC-----CGGAGGGTGC				: 464
Ghominis1 :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 474
Ghominis2 :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 475
Hfelis gb :	ANCTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 500
Hbizzozero :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 474
Hsalomonis :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 432
Abutzleri :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 520
Cjejuni gb :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 517
Wsuccinoge :	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				: 505
	AACTCCGTGCCagcagccgcggtataCGGAGGGTGC				

Figure 1 - 19

	*	720	*	740	
HbovisR2XA :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCTGT				: 508
Hpylori gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 542
Hbilis gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 712
Hcanis gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 532
Hcinaedi g :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 540
Hacinonych :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 541
Hnemestrin :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 538
Hcholescys :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 522
Hpmatensi :	NAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 542
Hmustelae :	NAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 541
Hrodentium :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 516
Hpullorum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 533
Hfennellia :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGCG				: 541
Htrogontum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 518
Hmuridarum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGCG				: 537
Hhepaticus :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGCG				: 501
Ghominis1 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGCG				: 511
Ghominis2 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGCG				: 512
Hfelis gb :	NAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGCG				: 537
Hbizzozero :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGCG				: 511
Hsalomonis :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGGCG				: 469
Abutzleri :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCTGT				: 557
Cjejuni gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGCGT				: 554
Wsuccinoge :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGGACGT				: 542
	AAGCGTTACTCGGAATCACTGGGCGTAAAGAG gcGt				

Figure 1 - 20

* 760 *

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HbovisR2XA : AGGCGGCAATGAAAGTCAGGCCTGAAATCCCGTGGCT : 545
Hpylori|gb : AGGCGGGATCAAGTCAGGTGTGAAATCCTTTGGCT : 579
Hbilis|gb| : AGGCGGCAGTAAGTCAGTGTGAAATCCTGTAGCT : 749
Hcanis|gb| : AGGCGGCAAGTAAGTCAGTGTGAAATCCTGTAGCT : 569
Hcinaedi|g : AGGCGGGTAGTCAAGTCAGTGTGAAATCCTGTAGCT : 577
Hacinonych : AGGCGGGRTTMAAGTCAGTGTGAAATCCTTTGGCT : 578
Hnemestrin : AGGCGGCATCAAGTCAGGTGTGAAATCCTTTGGCT : 575
Hcholescys : AGGCGGGGTAAAGTCAGTGTGAAATCCTTTGGCT : 559
Hpamatensi : AGGCGGGGTAAAGTCAGTGTGAAATCCTTTGGCT : 579
Hmustelae| : AGGCGGAGTAAAGTCAGTGTGAAATCCTGTAGCT : 578
Hrodentium : AGGCGGGATCAAGTCAGTGTGAAATCCTTTGGCT : 553
Hpullorum| : AGGCGGGGTAAAGTCAGTGTGAAATCCTTTGGCT : 570
Hfennellia : AGGCGGGATCAAGTCAGTGTGAAATGCTTTGGCT : 578
Htrogontum : AGGCGGGGTAAAGTCAGTGTGAAATCCTGTAGCT : 555
Hmuridarum : AGGCGGGCTAAAGTCAGTGTGAAATCCTTTAGCT : 574
Hhepaticus : AGGCGGGGTAAAGTCAGTGTGAAATCCTGTAGCT : 538
Ghominis1| : AGGCGGGAGGACAAGTCAGGTGTGAAATCCTTTGGCT : 548
Ghominis2| : AGGCGGGGTAAAGTCAGGTGTGAAATCCTTTGGCT : 549
Hfelis|gb| : AGGCGGGGTAAAGTCAGTGTGAAATCCTTTGGCT : 574
Hbizzozero : AGGCGGGGTAAAGTCAGGTGTGAAATCCTTTGGCT : 548
Hsalomonis : AGGCGGGGTAAAGTCAGTGTGAAATCCTTTGGCT : 506
Abutzleri| : AGGCGGATTAAAGCTTGAAGTCAAATCCTTTAGCT : 594
Cjejuni|gb : AGGCGGATTTCAGTCTCTTGTGAAATCTATGGCT : 591
Wsuccinoge : AGGCGGCCCTTCAAGTCAGTGTGAAATCTAAGCGCT : 579
AGGCGGg t aAGTcag tGTGAAATcct t GCT

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Figure 1 - 21

	780	*	800	*	
HbovisR2XA :	TAAC	TGCG	GAAGTGGG	TTTGAARCT	TCATTCTGGAG : 582
Hpylori gb :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 616
Hbilis gb :	TAAC	TAC	AGAACTGC	ATTGAAACT	TTTCTGGAG : 786
Hcanis gb :	TAAC	TAC	AGAACTGC	ATTGAAACT	TTTCTGGAG : 606
Hcinaedi g :	TAAC	TAC	AGAACTGC	ATTGAAACT	GACTATCTGGAG : 614
Hacinonych :	TNAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 615
Hnemestrin :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 612
Hcholescys :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 596
Hpamatensi :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 616
Hmustelae :	TAAC	TAC	AGAACTGC	ATTGAAACT	TTTCTGGAG : 615
Hrodentium :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 590
Hpullorum :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 607
Hfennellia :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 615
Htrogontum :	TAAC	TAC	AGAACTGC	ATTGAAACT	TTTCTGGAG : 592
Hmuridarum :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 611
Hhepaticus :	TAAC	TAC	AGAACTGC	ATTGAAACT	TTTCTGGAG : 575
Ghominis1 :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 585
Ghominis2 :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 586
Hfelis gb :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 611
Hbizzozero :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 585
Hsalomonis :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 543
Abutzleri :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 631
Cjejuni gb :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 628
Wsuccinoge :	TAAC	TA	AGAACTGC	ATTGAAACT	TTTCTGGAG : 616

TAAC a agAACTGCaTttgAAACT a tCT GAg

Figure 1 - 22

	820	*	840	*	
HbovisR2XA :	TATGGGAGAGG	CAGGTGGA	CTTGGGTAGGGGTA		: 619
Hpylori gb :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 653
Hbilis gb :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 823
Hcanis gb :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 643
Hcinaedi g :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 651
Hacinonych :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 652
Hnemestrin :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 649
Hcholescys :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 633
Hpamatensi :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 653
Hmustelae :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 652
Hrodentium :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 627
Hpullorum :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 644
Hfennellia :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 652
Htrogontum :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 629
Hmuridarum :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 648
Hhepaticus :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 612
Ghominis1 :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 622
Ghominis2 :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 623
Hfelis gb :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 648
Hbizzozero :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 622
Hsalomonis :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 580
Abützleri :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 668
Cjejuni gb :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 665
Wsuccinoge :	TATGGGAGAGGTAGGTGGAAT	TCTTGGGTAGGGGTA			: 653

T tGGGAGAGGTAGGTGGAATTcttGGGTAGGGGTA

Figure 1 - 23

	860	*	880	
HbovisR2XA :	AAATCCGTAGATATCAAG	AGAATACTCATTGCGAAG	:	656
Hpylori gb :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	690	
Hbilis gb :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	860	
Hcanis gb :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	680	
Hcinaedi g :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	688	
Hacinonych :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	689	
Hnemestrin :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	686	
Hcholescys :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	670	
Hpamatensi :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	690	
Hmustelael :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	689	
Hrodentium :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	664	
Hpullorum :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	681	
Hfennellia :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	689	
Htrogontum :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	666	
Hmuridarum :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	685	
Hhepaticus :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	649	
Ghominis1 :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	659	
Ghominis2 :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	660	
Hfelis gb :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	685	
Hbizzozero :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	659	
Hsalomonis :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	617	
Abutzleri :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	705	
Cjejuni gb :	AAATCCGTAGATATCAAGGAATACTCATTGCGAAG	:	702	
Wsuccinoge :	AAATCCGTAGAGATCAAGAGGAATACTCATTGCGAAG	:	690	

AAATCCGTAGAGATCAAGAgGAATACTcATTGCGAAG

Figure 1 - 24

	*	900	*	920	
HbovisR2XA :	GGGACCTGCTGGAACA	CACTGACGCTGAT	GC	CGA	: 692
Hpylori gb :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CTA	: 727
Hbilis gb :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 896
Hcanis gb :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 716
Hcinaedil g :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 724
Hacinonych :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 726
Hnemestrin :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 723
Hcholescys :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 706
Hpamatensi :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 726
Hmustelae :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 725
Hrodentium :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 700
Hpullorum :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 717
Hfennellia :	GNGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 725
Htrogontum :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 702
Hmuridarum :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 721
Hhepaticus :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 685
Ghominis1 :	GGGACCTGCTGGAACA	CACTGACGCTGAT	GC	CGA	: 696
Ghominis2 :	GGGACCTGCTGGAACA	CACTGACGCTGAT	GC	CGA	: 697
Hfelis gb :	GGGACCTGCTGGAACA	CACTGACGCTGAT	GC	CGA	: 721
Hbizzozero :	GGGACCTGCTGGAACA	CACTGACGCTGAT	GC	CGA	: 696
Hsalomonis :	GGGACCTGCTGGAACA	CACTGACGCTGAT	GC	CGA	: 654
Abutzleri :	GGGATCTGCTGGAACA	CACTGACGCTGAT	GC	CGA	: 741
Cjejuni gb :	GGGATCTGCTGGAACA	CACTGACGCTGAT	GC	CGA	: 738
Wsuccinoge :	GGGACCTGCTGGAACA	TACTGACGCTGAT	GC	CGA	: 726

GCGAcCTgCTGGAACa tActGACGCTgAt gc CgA

Figure 1 - 25

	*	940	*	960	
HbovisR2XA :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 729
Hpylori gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 764
Hbilis gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 933
Hcanis gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 752
Hcinaedi g :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 761
Hacinonych :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 763
Hnemestrin :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 760
Hcholescys :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 743
Hpamatsensi :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 763
Hmustelae :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 762
Hrodentium :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 737
Hpullorum :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 753
Hfennellia :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 762
Htrogontum :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 739
Hmuridarum :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 758
Hhepaticus :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 722
Ghominis1 :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 733
Ghominis2 :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 734
Hfelis gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 758
Hbizzozero :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 733
Hsalomonis :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 691
Abutzleri :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 778
Cjejuni gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 775
Wsuccinoge :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 763
	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				

Figure 1 - 26

	*	980	*	100	
HbovisR2XA :	TCCACGCCCTAAACGATG	GATGCTAATGCT	CGGGGGG	:	766
Hpylori gb :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	GAGGGG	:	801
Hbilis gb :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	CCCTG	:	970
Hcanis gb :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	CCCTG	:	789
Hcinaedilg :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	CCCTG	:	798
Hacinonych :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	GGRGG	:	800
Hnemestrin :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	GAGGG	:	797
Hcholescys :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	GGGTG	:	780
Hpamatensi :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	GTGGAG	:	800
Hmustelae :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	GGGTG	:	799
Hrodentium :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	GCGAG	:	774
Hpullorum :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	GTGAG	:	790
Hfennellia :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	CCCTG	:	799
Htrogontum :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	CCCTG	:	776
Hmuridarum :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	CCCTG	:	795
Hhepaticus :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	CCCTG	:	759
Ghominis1 :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	G-AGG	:	769
Ghominis2 :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	GGGGG	:	771
Hfelis gb :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	GGGGG	:	795
Hbizzozero :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	GGGGG	:	770
Hsalomonis :	TCCACGCCCTAAACGATG	GATGCTAGTTGTT	GGGGG	:	728
Abutzleri :	TCCACGCCCTAAACGATG	TACACTAGTTGTT	GTGAG	:	815
Cjejuni gb :	TCCACGCCCTAAACGATG	TACACTAGTTGTT	GGGTG	:	812
Wsuccinoge :	TCCACGCCCTAAACGATG	AATGCTAGTTGTT	CCCTG	:	800
	TCCACGCCCTAAACGATG AtgCTAgTTGTtG				G

Figure 1 - 27

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0          *          1020          *
HbovisR2XA : CTT-GTCTCCTGGGTAATGCAGCTAACGGCTTAAGCA : 802
Hpylori|gb : CTTASTCTCTCCAGTAATGCAGCTAACGGCTTAAGCA : 838
Hbilis|gb| : CTT-GTCAGGGCAGTAATGCAGCTAACGGCTTAAGCA : 1006
Hcanis|gb| : CTT-ETCAGGGCAGTAATGCAGCTAACGGCTTAAGCA : 825
Hcinaedi|g : CTT-NTCAGGGCAGTAATGCAGCTAACGGCTTAAGCA : 834
Hacinonych : CTTTGTCTCTCCAGTAATGCAGCTAACGGCTTAAGCA : 837
Hnemestrin : CTTASTCTCTCCAGTAATGCAGCTAACGGCTTAAGCA : 834
Hcholescys : CTT-GTCACTCCAGTAATGCAGCTAACGGCTTAAGCA : 816
Hpamatensi : CTT-GTCTCTGCAGTAATGCAGCTAACGGCTTAAGCA : 836
Hmustelae| : CTT-GTCACTCCAGTAATGCAGCTAACGGCTTAAGCA : 835
Hrodentium : CTT-GTCCTTGCAGTAATGCAGCTAACGGCTTAAGCA : 810
Hpullorum| : CTT-GTCCTTGCAGTAATGCAGCTAACGGCTTAAGCA : 826
Hfennellia : CTC-GTCAGGGCAGTAATGCAGCTAACGGCTTAAGCA : 835
Htrogontum : CTT-GTCAGGGCAGTAATGCAGCTAACGGCTTAAGCA : 812
Hmuridarum : CTT-GACAGGGCAGTAATGCAGCTAACGGCTTAAGCA : 831
Hhepaticus : CTT-GTCAGGGCAGTAATGCAGCTAACGGCTTAAGCA : 795
Ghominis1| : CTTTGTCTTTCCAGTAATGCAGCTAACGGCTTAAGCA : 806
Ghominis2| : CTTTGTCTCTCCAGTAATGCAGCTAACGGCTTAAGCA : 808
Hfelis|gb| : CTT-GTCCTCCAGTAATGCAGCTAACGGCTTAAGCA : 831
Hbizzozero : CTTTGTCCCCCAGTAATGCAGCTAACGGCTTAAGCA : 807
Hsalomonis : CTTTGTCCCCCAGTAATGCAGCTAACGGCTTAAGCA : 765
Abutzleri| : CTC-GACCTTGCAGTAATGCAGCTAACGGCTTAAGTG : 851
Cjejuni|gb : CTA-GCCATCTCAGTAATGCAGCTAACGGCTTAAGTG : 848
Wsuccinoge : CTT-GTCAGGGCAGTAATGCAGCTAACGGCTTAAGCA : 836
CTt GtC      CaGTAATGCAGcTAACgC TTAAGCa

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Figure 1 - 28

	1040	*	1060	*	
HbavisR2XA :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 839
Hpylori gb :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 875
Hbilis gb :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 1043
Hcanis gb :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 862
Hcinaedi g :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 871
Hacinonych :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 874
Hnemestrin :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 871
Hcholescys :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 853
Hpamatensi :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 873
Hmustelae :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 872
Hrodentium :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 847
Hpullorum :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 863
Hfennellia :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 872
Htrogontum :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 849
Hmuridarum :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 868
Hhepaticus :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 832
Ghominis1 :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 842
Ghominis2 :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 845
Hfelis gb :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 868
Hbizzozero :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 844
Hsalomonis :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 802
Abutzleri :	TACCGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 888
Cjejuni gb :	TACCGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 885
Wsuccinoge :	TCCTGGCTGGGGAGTACG		ATCGCAAGATTAAAACTCA		: 873
	T		CcGCCTGGGGAGTACGg		TCGCAAGATTAAAACTCA

Figure 1 - 29

	1080	*	1100	*	
HbovisR2XA :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 876
Hpylori gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 912
Hbilis gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 1080
Hcanis gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 899
Hcinaedi g :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 908
Hacinonych :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 911
Hnemestrin :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 908
Hcholescys :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 890
Hpamatensi :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 910
Hmustelae :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 909
Hrodentium :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 884
Hpullorum :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 900
Hfennellia :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 909
Htrogontum :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 886
Hmuridarum :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 905
Hhepaticus :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 869
Ghominis1 :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 878
Ghominis2 :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 882
Hfelis gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 905
Hbizzozero :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 881
Hsalomonis :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 839
Abutzleri :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 925
Cjejuni gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 922
Wsuccinoge :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				: 910
	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				

Figure 1 - 30

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	1120	*	1140		
HbovisR2XA :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	913	
Hpylori gb :	GTGGTTTAAATTCGANNNNAC	CGAAGAACCCTTACCTA	:	949	
Hbilis gb :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	1117	
Hcanis gb :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	936	
Hcinaedi g :	GTGGTTTAAATTCGA	GTATAC	CGAAGAACCCTTACCTA	:	945
Hacinonych :	GTGGTTTAAATTCGANNNNNN	CGAAGAACCCTTACCTA	:	948	
Hnemestrin :	GTGGTTTAAATTCGAAG	GTAC	CGAAGAACCCTTACCTA	:	945
Hcholescys :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	927	
Hpamatensi :	GTGGTTTAAATTCGANNNNTAC	CGAAGAACCCTTACCTA	:	947	
Hmustelae :	GTGGTTTAAATTCGANNNNTAC	CGAAGAACCCTTACCTA	:	946	
Hrodentium :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	921	
Hpullorum :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	937	
Hfennellia :	GTGGTTTAAATTCGAANNNTAC	CGAAGAACCCTTACCTA	:	946	
Htrogontum :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	923	
Hmuridarum :	GTGGTTTAAATTCGANNNNNAC	CGAAGAACCCTTACCTA	:	942	
Hhepaticus :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	906	
Ghominis1 :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	915	
Ghominis2 :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	919	
Hfelis gb :	GTGGTTTAAATTCGANNNNNNN	CGAAGAACCCTTACCTA	:	942	
Hbizzozero :	GTGGTTTAAATTCGAAGATAC	CGAAGAACCCTTACCTA	:	918	
Hsalomonis :	GTGGTTTAAATTCGAT	GTCTAC	CGAAGAACCCTTACCTA	:	876
Abutzleri :	GTGGTTTAAATTCGANNNNNAC	CGAAGAACCCTTACCTG	:	962	
Cjejuni gb :	GTGGTTTAAATTCGAAGNTAC	CGAAGAACCCTTACCTG	:	959	
Wsuccinoge :	GTGGTTTAAATTCGANNNNNAC	CGAAGAACCCTTACCTG	:	947	
	GTGGTTTAAATTCGAagaTAC CGAAGAACCCTTACCTa				

Figure 1 - 31

	*	1160	*	1180	
HbovisR2XA :	GGCTTGACATTGA	GGAATC	ACCCGAA	AGCTGGAG	: 950
Hpylori gb :	GGCTTGACATTGA	GAGAATCC	CTAGA	AATAGTGGAG	: 986
Hbilis gb :	GGCTTGACATTGA	AGAATCC	CTAGA	AATAGTGGAG	: 1154
Hcanis gb :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGCGGAG	: 973
Hcinaedi g :	GGCTTGACATTGA	AGAATCC	CTAGA	AATAGTGGAG	: 982
Hacinonych :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGTGGAG	: 985
Hnemestrin :	GGCTTGACATTGA	GAGAATCC	CTAGA	AATAGTGGAG	: 982
Hcholescys :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGCGGAG	: 964
Hpamatensi :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGCGGAG	: 984
Hmustelae :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGCGGAG	: 983
Hrodentium :	GGCTTGACATTGA	AGAATCC	CTAGA	AATAGTGGAG	: 958
Hpullorum :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGCGGAG	: 974
Hfennellia :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGCGGAG	: 983
Htrogontum :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGCGGAG	: 960
Hmuridarum :	GGCTTGACATTGA	AGAATCCTATAGA	ATATGGGAG		: 979
Hhepaticus :	GGCTTGACATTGA	AGAATC	CTAGA	AATAGTGGAG	: 943
Ghominis1 :	GGCTTGACATTGA	AGGAATCC	CTAGA	AATAGGGGAG	: 952
Ghominis2 :	GGCTTGACATTGA	AGGAATC	CTAGA	AATAGCGGAG	: 956
Hfelis gb :	GGCTTGACATTGA	ANGAATC	CTAGA	AATAGTGGAG	: 979
Hbizzozero :	GGCTTGACATTGA	AGGAATCCC	CTAGA	AATAGGGGAG	: 955
Hsalomonis :	GGCTTGACATTGA	AGGAATC	CTAGA	AATAGCGGAG	: 913
Abutzleri :	GACTTGACATAG	AAGAATGATT	TAGA	AATAGATTAG	: 999
Cjejuni gb :	GGCTTGATAT	CCTAAGAAC	CTATAGA	ATATGAGGG	: 996
Wsuccinoge :	GGCTTGACATTGA	AGAATC	CTATAGA	ATATGGGAG	: 984

GgCTTGAcAttga aGAAtc ctagA Atag ggaG

Figure 1 - 32

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      *           1200           *           1220
HbovisR2XA : TG-CCAGTTTACGGAGGCTGAAAACAGGTGCTGCAC : 986
Hpylori|gb : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 1023
Hbilis|gb| : TG-CTGGCTTCCGAGGCTGAAACAGGTGCTGCAC : 1190
Hcanis|gb| : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 1010
Hcinaedi|g : TG-TTGGCTTCCGAGGCTGAAAACAGGTGCTGCAC : 1018
Hacinonych : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 1022
Hnemestrin : TGTCTGGCTTACAAATCTGAAAACAGGTGCTGCAC : 1019
Hcholescys : TG-CTGGCTTCCGAGGCTGAAAACAGGTGCTGCAC : 1000
Hpamatensi : TG-CTGGCTTCCGAGGCTGAAAACAGGTGCTGCAC : 1020
Hmustelae| : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 1020
Hrodentium : TG-CTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 994
Hpullorum| : TG-CTGGCTTCCGAGGCTGAAAACAGGTGCTGCAC : 1010
Hfennellia : TG-CTGGCTTCCGAGGCTGAAAACAGGTGCTGCAC : 1019
Htrogontum : TG---CCCTTCGGGGAGGCTGAAAACAGGTGCTGCAC : 994
Hmuridarum : TG-CCACTTCTGTTGGAGCTGAAAACAGGTGCTGCAC : 1015
Hhepaticus : TG----CCTTCGGGGAGGCTGAAAACAGGTGCTGCAC : 976
Ghominis1| : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 989
Ghominis2| : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 993
Hfelis|gb| : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 1016
Hbizzozero : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 992
Hsalomonis : TGTCTAGCTTCTGGACCTGAAAACAGGTGCTGCAC : 950
Abutzleri| : TG-TCTGCTTCAGAAACTTCCATACAGGTGCTGCAC : 1035
Cjejuni|gb : TG-CTAGCTTCTGGACCTGAGAGACAGGTGCTGCAC : 1032
Wsuccinoge : TG-CCGGTTTACGGAGGCTGAAAACAGGTGCTGCAC : 1020
TG c gcTt c gA C TgaAaACAGGTGCTGCAC

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Figure 1 - 33

	*	1240	*	12	
HbovisR2XA :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1023
Hpylori gb :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1060
Hbilis gb :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1227
Hcanis gb :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1047
Hcinaedi g :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1055
Hacinonych :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1059
Hnemestrin :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1056
Hcholescys :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1037
Hpamatensi :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1057
Hmustelae :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1057
Hrodentium :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1031
Hpullorum :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1047
Hfennellia :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1056
Htrogontum :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1031
Hmuridarum :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1052
Hhepaticus :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1013
Ghominis1 :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1026
Ghominis2 :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1030
Hfelis gb :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1053
Hbizzozero :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1029
Hsalomonis :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 987
Abutzleri :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1072
Cjejuni gb :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1069
Wsuccinoge :	GGCTGTCGTCAGCTCGTGTGCTGAGATGTTGGGTTAA				: 1057

Figure 1 -34

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60          *          1280          *
HbovisR2XA : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1060
Hpylori|gb : GTCCCGCAACGAGCGCAACCCCTTTTCTTACTTGCTA : 1097
Hbilis|gb| : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1264
Hcanis|gb| : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1084
Hcinaedi|g : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1092
Hacinonych : GTCCCGCAACGAGCGCAACCCCTTTTCTTACTTGCTA : 1096
Hnemestrin : GTCCCGCAACGAGCGCAACCCCTTTTCTTACTTGCTA : 1093
Hcholescys : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1074
Hpamatensi : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1094
Hmustelae| : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1094
Hrodentium : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1068
Hpullorum| : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1084
Hfennellia : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1093
Htrogontum : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1068
Hmuridarum : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1089
Hhepaticus : N----- : 1015
Ghominis1| : GTCCCGCAACGAGCGCAACCCCTTTTCTTACTTGCTA : 1063
Ghominis2| : GTCCCGCAACGAGCGCAACCCCTTTTCTTACTTGCTA : 1067
Hfelis|gb| : GTCCCGCAACGAGCGCAACCCCTTTTCTTACTTGCTA : 1090
Hbizzozero : GTCCCGCAACGAGCGCAACCCCTTTTCTTACTTGCTA : 1066
Hsalomonis : GTCCCGCAACGAGCGCAACCCCTTTTCTTACTTGCTA : 1024
Abutzleri| : GTCCCGCAACGAGCGCAACCCCTCCTTACTTGCTA : 1109
Cjejuni|gb : GTCCCGCAACGAGCGCAACCCCTATTTACTTGCTA : 1106
Wsuccinoge : GTCCCGCAACGAGCGCAACCCCTCACCTAGTTGCTA : 1094
Gtcccgcaacgagcgcaaccctc t cttagtgtgcta

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Figure 1 - 35

```

      1300      *      1320      *
HbovisR2XA : TCAGTT -GCTGGGCACTCTAAGAGACTGCCTCG : 1096
Hpylori|gb : ACAGGTTATGCTGAGAACTCTAAGATACTGCCTCCG : 1134
Hbilis|gb| : GCAGTT -GCTGAGCACTCTAAGAGACTGCCTCG : 1300
Hcanis|gb| : GCAGTT -GCTGAGCACTCTAAGAGACTGCCTCG : 1120
Hcinaedi|g : GCAGCT -GCTGAGCACTCTAAGAGACTGCCTCG : 1128
Hacinonych : ACAGGTAWGCTGAGAACTCTAAGAGACTGCCTCCG : 1133
Hnemestrin : ACAGGKATGCTGAGAACTCTAAGATACTGCCTCCG : 1129
Hcholescys : GCAGTT -GCTGAGCACTCTAAGAGACTGCCTCG : 1110
Hpamatensi : ACAGGTT -GCTGAGCACTCTAAGAGACTGCCTCG : 1130
Hmustelae| : GCAGTT -GCTGAGCACTCTAAGAGACTGCCTCG : 1130
Hrodentium : ACTAAT -GTAGAGCACTCTAAGAGACTGCCTCG : 1104
Hpullorum| : GCAGTT -GCTGAGCACTCTAAGAGACTGCCTCG : 1120
Hfennellia : GCAGTT -GCTGAGCACTCTAAGAGACTGCCTCG : 1129
Htrogontum : GCAGTT -GCTGAGCACTCTAAGAGACTGCCTCG : 1104
Hmuridarum : GCAGTTAGCTGAGCACTCTAAGAGACTGCCTCG : 1126
Hhepaticus : -----NNNNNNNNNN----- : 1027
Ghominis1| : ACAGGTTATGCTGCGCACTCTAAGAGACTGCCTGCG : 1100
Ghominis2| : ACAGGTGATGCTGAGCTCTCTAAGAGACTGCCTGCG : 1104
Hfelis|gb| : ACAGGTAETGCTGAGCTCTCTAAGATACTGCCTGCG : 1127
Hbizzozero : ACAGGTAAAGCTGAGCTCTCTAAGATACTGCCTGCG : 1103
Hsalomonis : ACAGGTAETGCTGAGCTCTCTAAGATACTGCCTGCG : 1061
Abutzleri| : ACAGET -GCTGAGAACTCTAAGAGACTGCCTACG : 1145
Cjejuni|gb : ACGGTT -GCCGAGCACTCTAAATAGACTGCCTCG : 1142
Wsuccinoge : ACGGTT -GCCGAGCACTCTAGTAGACTGCCTCG : 1130
      cag t      gctgagcaCTCTAag Agactgcct cg

```

Figure 1 - 36

	1340	*	1360	
HbavisR2XA :	TAAGTAGGAGGAAGGCGAGGATGACGTCAGTCATCA			: 1133
Hpylori gb :	TAAGTAGGAGGAAGGTCGGACGACGTCAGTCATCA			: 1171
Hbilis gb :	TAAGTAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1337
Hcanis gb :	TAAATAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1157
Hcinaedi g :	TAAATAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1165
Hacinonych :	TAAATAGGAGGAAGGTCGGACGACGTCAGTCATCA			: 1170
Hnemestrin :	TAAATAGGAGGAAGGTCGGACGACGTCAGTCATCA			: 1166
Hcholescys :	TAAATAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1147
Hpmatensi :	TNAGTAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1167
Hmustelael :	TNAGTAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1167
Hrodentium :	CAAGTAGGAGGAAGGTCAGGATGACGTCAGTCATCA			: 1141
Hpullorum :	TAAGTAGGAGGAAGGTCAGGATGACGTCAGTCATCA			: 1157
Hfennellia :	CANGTAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1166
Htrogonium :	TAAGTAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1141
Hmuridarum :	TAAGTAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1163
Hhepaticus :	-----NNNNNNNNNNNNNNNNNNNNNNNNNNNN-----			: 1053
Hghominis1 :	TAAATAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1133
Hghominis2 :	TAAATAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1141
Hfelis gb :	TAAATAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1164
Hbizzozero :	TAAATAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1140
Hsalomonis :	TAAATAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1098
Abutzleri :	CAAGTAGGAGGAAGGTCAGGATGACGTCAGTCATCA			: 1182
Cjejun gb :	TNAGTAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1179
Wsuccinoge :	CAAGTAGGAGGAAGGTCAGGACGACGTCAGTCATCA			: 1167
	taaG aqgAGGAAGGtGaGGAcGACGTcAagtcatca			

Figure 1 - 37

```

      *           1380           *           1400
HbovisR2XA : TGGCCCTTATGTCGCGGGCTACGCACGTGCTACAATG : 1170
Hpylori|gb : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1208
Hbilis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1374
Hcanis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hcinaedi|g : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1202
Hacinonych : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1207
Hnemestrin : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Hcholescys : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1184
Hpamatensi : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hmustelae| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1204
Hrodentium : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hpullorum| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1194
Hfennellia : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1203
Htrogontum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1178
Hmuridarum : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1200
Hhepaticus : -----N-----MNE : 1057
Ghominis1| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1170
Ghominis2| : TGGCCCTTACNCCTAGGGCTACACACGTGCTACAATG : 1178
Hfelis|gb| : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1201
Hbizzozero : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1177
Hsalomonis : TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG : 1135
Abutzleri| : TGGCCCTTACGTCCAGGGCTACACACGTGCTACAATG : 1219
Cjejuni|gb : TGGCCCTTATGCCAGGGCGACACACGTGCTACAATG : 1216
Wsuccinoge : TGGCCCTTACGCCYAGGGCTACACACGTGCTACAATG : 1204
          tggcccttAcgcctagggctacacacgtgctacaATG

```

Figure 1 - 38

	*	1420	*	1440	
HbovisR2XA :	CGA	CTACAAAGAGATGCAATGTCTA	ATGGAGC	:	1207
Hpylori gb :	GG	GACAAAGAGAAGCAAT	TCTG	AGTGGAGCC	: 1245
Hbilis gb :	CGACAT	ACAAAGAGATGCAAT	TCTG	AGTGGAGCC	: 1411
Hcanis gb :	CG	CATACAAATGAGGAGCAAT	TCTG	AGTGGAGCC	: 1231
Hcinaedi g :	CGACAT	ACAAAGAGATGCAAT	TCTG	AGTGGAGCC	: 1239
Hacinonych :	CG	GACAAAGAGAGAGGAT	TCTG	AGTGGAGCC	: 1244
Hnemestrin :	GG	GACAAAGAGAGAGCAAT	TCTG	AGTGGAGCC	: 1240
Hcholescys :	GTA	GTACAAAGAGAGAGCAAT	TCTG	AGTGGAGCC	: 1221
Hpamatensi :	GGA	GACAAAGAGAGAGCAAT	TCTG	AGTGGAGCC	: 1241
Hmustelae :	GG	GACAAAGAGAGAGCAAT	TCTG	AGTGGAGCC	: 1241
Hrodentium :	GGAAGT	ACAAAGAGATGCAAT	TTCTG	AATGGAGCC	: 1215
Hpullorum :	GG	GTACAAAGAGAGAAGCAAT	TCTG	AGTGGAGCC	: 1231
Hfennellia :	GG	GACAAAGAGAGAAGCAAT	TCTG	AGTGGAGCC	: 1240
Htrogontum :	GG	CGACAAAGAGAGAGCAAT	TCTG	AGTGGAGCC	: 1215
Hmuridarum :	GG	CTGACAAAGAGAGAGCAAT	TCTG	AGTGGAGCC	: 1237
Hhepaticus :	NNNN	NNNNNNNNNNNNNNNNNNNN	NNNN	NNNNNNNN	: 1094
Ghominis1 :	GG	GACAAAGAGATGCAAG	TCTG	AGTGGAGCC	: 1207
Ghominis2 :	GGA	GACAAAGAGATGCAATG	TCTG	AGTGGAGCC	: 1215
Hfelis gb :	GG	GACAAAGAGATGCAATG	TCTG	AGTGGAGCC	: 1238
Hbizzozero :	GGA	GACAAAGAGATGCAATG	TCTG	AGTGGAGCC	: 1214
Hsalomonis :	GG	CGACAAAGAGATGCAATG	TCTG	AGTGGAGCC	: 1172
Abutzleri :	GG	ATACAAAGAGAGAGCAAT	TCTG	AGTGGAGCC	: 1256
Cjejuni gb :	GCA	ATACAAATGAGAGCAAT	TCTG	AGTGGAGCC	: 1253
Wsuccinoge :	GT	CTACAAAGAGAAGCAAT	TCTG	AGTGGAGCC	: 1241
	Gg	g ACAAagAGa GCaAt	G	gA gtgGAGC	

Figure 1 - 39

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          *          1460          *          1480
HbovisR2XA : AAACCTTAAAAACCTCTCCAGTTCGGATTG GGTCTG : 1244
Hpylori|gb : AATCTTCAAAACCTCTCAGTTCGGATTG AGGCTG : 1282
Hbilis|gb| : AATCTTAAAAATGCTCTCAGTTCGGATTG AGCTG : 1448
Hcanis|gb| : AATCTTAAAAATGCTCTCAGTTCGGATTG AGCTG : 1268
Hcinaedi|g : AATCTTAAAAATGCTCTCAGTTCGGATTG AGCTG : 1276
Hacinonych : AATCTTCAAAACCTCTCCAGTTCGGATTG CAGGCTG : 1281
Hnemestrin : AATCTTAAAAACGCTCTCAGTTCGGATTG CAGGCTG : 1277
Hcholescys : AATCTTAAAAACCTCTCAGTTCGGATTG AGCTG : 1258
Hpamatensi : AATCTTAAAAACCTCTCAGTTCGGATTG AGCTG : 1278
Hmustelae| : AATCTTAAAAACCTCTCAGTTCGGATTG AGCTG : 1278
Hrodentium : AATCTTAAAAACTCTCTCAGTTCGGATTG AGCTG : 1252
Hpullorum| : AATCTTAAAAACCTCTCAGTTCGGATTG AGCTG : 1268
Hfennellia : AATCTTAAAAACGCTCTCAGTTCGGATTG AGCTG : 1277
Htrogontum : AATCTTAAAAACGCTCTCAGTTCGGATTG AGCTG : 1252
Hmuridarum : AATCTTAAAAACGCTCTCAGTTCGGATTG AGCTG : 1274
Hhepaticus : NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN : 1131
Ghominis1| : AATCTTATAAAACCTCTCTAGTTCGGATTG CAGGCTG : 1244
Ghominis2| : AATCTTAAAAACCTCTCAGTTCGGATTG AGGCTG : 1252
Hfelis|gb| : AATCTTAAAAACCTCTCAGTTCGGATTG CAGGCTG : 1275
Hbizzozero : AATCTTAAAAACCTCTCAGTTCGGATTG CAGGCTG : 1251
Hsalomonis : AATCTTAAAAACGCTCTCAGTTCGGATTG CAGGCTG : 1209
Abutzleri| : AATCTTAAAAATGCTCTCCAGTTCGGATTG AGCTG : 1293
Cjejuni|gb : AATCTTAAAAATGTCTCCAGTTCGGATTG TCCTG : 1290
Wsuccinoge : AATCTTTAAAAACCATCTCAGTTCGGATTG AGCTG : 1278
AAtCT AAAAC cTCTcAGTTCGGATTG ag CTG

```

Figure 1 - 40

	*	1500	*	1	
HbovisR2XA :	CAACTCG	CC	CATGAAGCA	GGAATCGCTAGTAATCG	: 1281
Hpylori gb :	CAACTCG	CCTG	CATGAAGCTGGAATCGCTAGTAATCG		: 1319
Hbilis gb :	CAACTCG	CT	CAT	AAAGCTGGAATCGCTAGTAATCG	: 1485
Hcanis gb :	CAACTCG	CT	CATGAAGCTGGAATCGCTAGTAATCG		: 1305
Hcinaedi g :	CAACTCG	CT	CAT	AAAGCTGGAATCGCTAGTAATCG	: 1313
Hacinonych :	CAACTCG	CCTG	CATGAAGCC	GGAATCGCTAGTAATCG	: 1318
Hnemestrin :	CAACTCG	CCTG	CATGAAGCTGGAATCGCTAGTAATCG		: 1314
Hcholescys :	CAACTCG	CT	CATGAAGCTGGAATCGCTAGTAATCG		: 1295
Hpamatensi :	CAACTCG	CT	CATGAAGCTGGAATCGCTAGTAATCG		: 1315
Hmustelae :	CAACTCG	CT	CATGAAGCTGGAATCGCTAGTAATCG		: 1315
Hrodentium :	CAACTCG	CT	CATGAAGCTGGAATCGCTAGTAATCG		: 1289
Hpullorum :	CAACTCG	CT	CATGAAGCTGGAATCGCTAGTAATCG		: 1305
Hfennellia :	CAACTCG	CT	CAT	AAAGCTGGAATCGCTAGTAATCG	: 1314
Htrogontum :	CAACTCG	CT	CAT	AAAGCTGGAATCGCTAGTAATCG	: 1289
Hmuridarum :	CAACTCG	CT	CATGAAGCTGGAATCGCTAGTAATCG		: 1311
Hhepaticus :	NNNNNNNN	NN	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN		: 1168
Ghominis1 :	CAACTCG	CCTG	CATGAAGCTGGAATCGCTAGTAATCG		: 1281
Ghominis2 :	CAACTCG	CCTG	CATGAAGCTGGAATCGCTAGTAATCG		: 1289
Hfelis gb :	CAACTCG	CCTG	CATGAAGCTGGAATCGCTAGTAATCG		: 1312
Hbizzozero :	CAACTCG	CCTG	CATGAAGCTGGAATCGCTAGTAATCG		: 1288
Hsalomonis :	CAACTCG	CCTG	CATGAAGCTGGAATCGCTAGTAATCG		: 1246
Abutzleri :	CAACTCG	CT	CATGAAGT	TGGAATCGCTAGTAATCG	: 1330
Cjejuni gb :	CAACTCG	GAG	CATGAAGCC	GGAATCGCTAGTAATCG	: 1327
Wsuccinoge :	CAACTCG	CT	CATGAAGCTGGAATCGCTAGTAATCG		: 1315
	CAACTCG	ct	CATGAAGctGGAATCGCTAGTAATCG		

Figure 1 - 4|

	520	*	1540	*	
HbovisR2XA :	TGAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1318		
Hpylori gb :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1356		
Hbilis gb :	TGAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1522		
Hcanis gb :	TGAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1342		
Hcinaedilg :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1350		
Hacinonych :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1355		
Hnemestrin :	CTATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1351		
Hcholescys :	TGAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1332		
Hpamatensi :	TGAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1352		
Hmustelae :	TGAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1352		
Hrodentium :	TTGATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1326		
Hpullorum :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1342		
Hfennellia :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1351		
Htrogontum :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1326		
Hmuridarum :	TGAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1348		
Hhepaticus :	NAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1205		
Ghominis1 :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1318		
Ghominis2 :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1326		
Hfelis gb :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1349		
Hbizzozero :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1325		
Hsalomonis :	CAATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1283		
Abutzleri :	TTGATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1367		
Cjejuni gb :	TTGATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1364		
Wsuccinoge :	TTGATCAGCAATGTCACGGTGAATACGTTCCCGGGTC	:	1352		

aATCAGC ATGt CCGTGAATACGTTCCCGGGTC

Figure 1 - 42

```

      1560          *          1580          *
HbovisR2XA : TTGTACTCACCAA---TCAC----- : 1335
Hpylori|gb : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTGTT : 1393
Hbilis|gb| : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTATT : 1559
Hcanis|gb| : TTGTACTCACCGGCCCGTCACACCATGGGAGTTGTATT : 1379
Hcinaedi|g : TTGTACTCACCGGCCCGTCACACCATGGGAGTTGTATT : 1387
Hacinonych : TTGTACTCACCGGCCCGTCACACCATGGGAGTTGTGTT : 1392
Hnemestrin : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTGTT : 1388
Hcholescys : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTATT : 1369
Hpamatensi : TTGTACTCACCGGCCCGTCACACCATGGGAGTTGTATT : 1389
Hmustelae| : TTGTACTCACCGGCCCGTCACACCATGGGAGTTGTATT : 1389
Hrodentium : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTATT : 1363
Hpullorum| : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTATT : 1379
Hfennellia : TTGTACTCACCGGCCCGTCACACCATGGGAGTTGTATT : 1388
Htrogontum : TTGTACTCACCGGCCCGTCACACCATGGGAGTTGTATT : 1363
Hmuridarum : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTATT : 1385
Hhepaticus : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTATT : 1242
Ghominis1| : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTGTT : 1355
Ghominis2| : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTGTT : 1363
Hfelis|gb| : TTGTACTCACCGGNCCGTCACACCATGGGAGTTGTGTT : 1386
Hbizzozero : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTGTT : 1362
Hsalomonis : TTGTACTC----- : 1290
Abutzleri| : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGCACT : 1404
Cjejuni|gb : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGATTT : 1401
Wsuccinoge : TTGTACTCACCCCCCCGTCACACCATGGGAGTTGTATT : 1389
TTGTACTcaccgccccgtcacaccatgggagttgt tt

```

Figure 1 - 43

EP 1 035 219 A1

	1600	*	1620	
HbovisR2XA :	-----			-
Hpylori gb :	TGCCTTAAG	CAG	ATCTAAATTGGT	TACTGCCAC : 1430
Hbilis gb :	GCCTTAAG	C	GATACTAAATTGGT	TACCGCCAC : 1596
Hcanis gb :	GCCTTAAG	C	GATACTAAATTGGT	----- : 1406
Hcinaedi g :	GCCTTAAG	C	GATACTAAATTGGT	TANCGCCAC : 1424
Hacinonych :	TGCCTTAAG	CAG	ATCTAAAGCAG	TACTGCCAC : 1429
Hnemestrin :	TGCCTTAAG	A	GATCTAAATTACGT	TACTGCCAC : 1425
Hcholescys :	GCCTTAAGCC	G	ATCTAAACTGG	TACGTCCAC : 1406
Hpamatensi :	GCCTTAAGCC	G	ATCTAAACTGG	TACGTCCAC : 1426
Hmustelae :	GCCTTAAGCC	G	ATCTAAATTGG	TACGTCCAN : 1426
Hrodentium :	GCCTTAAG	C	GATCTAAACTGG	TACGTCCAC : 1400
Hpullorum :	GCCTTAAG	C	GATCTAAACTAGT	TANCGCCAC : 1416
Hfennellia :	GCCTTAAGCC	G	ATCTAAATTGG	TACGTCCAC : 1425
Htrogontum :	GCCTTAAG	C	GATCTAAACTGG	TACGTCCAC : 1400
Hmuridarum :	GCCTTAAG	C	GATACTAATTGGT	TACGTCCAC : 1422
Hhepaticus :	GCCTTAAG	C	GATACTAAATTGGT	TACGTCCAC : 1279
Ghominis1 :	TGCCTTAAG	CAG	ATCTAAAGCAG	TACTGCCAC : 1392
Ghominis2 :	TGCCTTAAG	CAG	ATCTAAAGCAG	TACTGCCAC : 1400
Hfelis gb :	TGCCTTAAG	CAG	ATCTAAGGTAG	TACTGCCAC : 1423
Hbizzozero :	TGCCTTAAG	CAG	ATCTAAGGTAG	TACTGCCAC : 1399
Hsalomonis :	-----			-
Abutzleri :	CATT	CGAAGCG	GGATCTAAAGTAG	TACGTCCAC : 1441
Cjejuni gb :	ACT	CGAAGCC	GAATACTAACTAGT	TACGTCCAC : 1438
Wsuccinoge :	GCCTTAAGCC	G	ATCTAAACTGG	TACGTCCAC : 1426
	gccttaag c g at ctaaa t g tac g ccac			

Figure 1 - 44

EP 1 035 219 A1

	*	1640	*	1660	
HbovisR2XA :	-----				-
Hpylori gb :	GCACACACAGCGACTGGG				: 1450
Hbilis gb :	GCATGCAGCGACTGGG				: 1616
Hcanis gb :	-----				-
Hcinaedi g :	GCATGCAGCGACTGGG				: 1444
Hacinonych :	GCACACACAGCGACTGGG				: 1449
Hnemestrin :	GCACACACAGCGACTGGG		TGAAGTCGTAACAAGGT		: 1462
Hcholescys :	GCATGCAGCGACTGGG				: 1425
Hpamatensi :	GCATGCAGCGACTGGG				: 1446
Hmustelae :	GCATNC				: 1435
Hrodentium :	GCATGCAGCGACTGGG		TGA		: 1423
Hpullorum :	GCATGCAGC				: 1428
Hfennellia :	GCATGCAGCGACTGGG				: 1445
Htrogontum :	GCATGCAGCGACTGGG		TG		: 1422
Hmuridarum :	GCATGCAGCGACTGGG				: 1442
Hhepaticus :	GCATGCAGCGACTGGG		TGA		: 1302
Ghominis1 :	GCACACACAGCGACTGGG		TG		: 1414
Ghominis2 :	GCACACACAGCGACTGGG		TG		: 1422
Hfelis gb :	GCACACACAGCGACTGGG				: 1443
Hbizzozero :	GCACACACAGCGACTGGG		TG		: 1421
Hsalomonis :	-----				-
Abutzleri :	AGTGGATTGAGYGACTGGG				: 1461
Cjejuni gb :	AGTGGATTGAGCGACTGGG				: 1458
Wsuccinoge :	GCATGCAGCGACTGGG				: 1446

gc a cagcgactggg

Figure 1 - 45

*

HbovisR2XA :	----- :	-
Hpylori gb :	----- :	-
Hbilis gb :	----- :	-
Hcanis gb :	----- :	-
Hcinaedi g :	----- :	-
Hacinonych :	----- :	-
Hnemestrin :	A----- :	1463
Hcholescys :	----- :	-
Hpamatensi :	----- :	-
Hmustelae :	----- :	-
Hrodentium :	----- :	-
Hpullorum :	----- :	-
Hfennellia :	----- :	-
Htrogontum :	----- :	-
Hmuridarum :	----- :	-
Hhepaticus :	----- :	-
Ghominis1 :	----- :	-
Ghominis2 :	----- :	-
Hfelis gb :	----- :	-
Hbizzozero :	----- :	-
Hsalomonis :	----- :	-
Abutzleri :	----- :	-
Cjejuni gb :	----- :	-
Wsuccinoge :	----- :	-

Figure 1 - 46

	*	20	*	
Hsuis2BXA0 :	-----			-
Ghominis1 :	-----		AGTGAACGCT	10
Ghominis2 :	-----		AGTGAACGCT	10
Hfelis gb :	TTTATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	37
Hbizzozero :	-----		AGTGAACGCT	10
Hbilis gb :	-----	ACTTGAACGCTGAG	CAGAGTGAACGCT	28
Hsalomonis :	-----			-
Hpylori gb :	TTTATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	37
Hcanis gb :	-----		CAGAGTGAACGCT	28
Hcinaedilg :	-TTATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	36
Hacinonych :	TTTATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	37
Hnemestrin :	NNTATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	37
Hcholescys :	-----		CAGAGTGAACGCT	18
Hpamatensi :	-TTATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	36
Hmustelae :	ATTATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	37
Hrodentium :	-----		CAGAGTGAACGCT	14
Hpullorum :	-----		CAGAGTGAACGCT	29
Hfennellia :	TTTACGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	37
Htrogontum :	-----		CAGAGTGAACGCT	14
Hmuridarum :	---ATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	34
Hhepaticus :	-----		CAGAGTGAACGCT	13
Abutzleri :	---ATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	34
Cjejuni gb :	--TATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	35
Wsuccinoge :	-TTATGGAG	CTTTCAGCGGCT	CAGAGTGAACGCT	36

cagagtgaacgct

Figure 2 - 1

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	40	*	60	*	
Hsuis2BXA0 :	-----TGC AAGTCGAACGATGAAG				: 19
Ghominis1 :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 47
Ghominis2 :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 47
Hfelis gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 74
Hbizzozero :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 47
Hbilis gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 65
Hsalomonis :	-----GAAG				: 4
Hpylori gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 74
Hcanis gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 65
Hcinaedi g :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 73
Hacinonych :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 74
Hnemestrin :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 74
Hcholescys :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 55
Hpamateni :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 73
Hmustelae :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 74
Hrodentium :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 51
Hpullorum :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 66
Hfennellia :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 74
Htrogontum :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 51
Hmuridarum :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 71
Hhepaticus :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 50
Abutzleri :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 71
Cjejuni gb :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 72
Wsuccinoge :	GGCGGCGTGCCTAATACATGCAAGTCGAACGATGAAG				: 73
	ggcggcgctgcctaatacatgcaagtcgaacgatgAag				

Figure 2 -2

	80	*	100	*	
Hsuis2BXA0 :	C--C-TAGCTTGCTAG	---	GTT--	GATTAGTGGCGCA	: 48
Ghominis1 :	C--C-TAGCTTGCTAG	---	TT--	GATTAGTGGCGCA	: 75
Ghominis2 :	C--C-TAGCTTGCTAG	---	GTG--	GATTAGTGGCGCA	: 76
Hfelis gb :	C--C-TAGCTTGCTAG	---	GCG--	GATTAGTGGCGCA	: 103
Hbizzozero :	C--C-TAGCTTGCTAG	---	GTG--	GATTAGTGGCGCA	: 76
Hbilis gb :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 98
Hsalomonis :	C--C-TAGCTTGCTAG	---	GCG--	GATTAGTGGCGCA	: 33
Hpylori gb :	CTTC-TAGCTTGCTAG	AGTGCT--		GATTAGTGGCGCA	: 108
Hcanis gb :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 98
Hcinaedilg :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 106
Hacinonych :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 107
Hnemestrin :	CTCT-AAGCTTGC	----	ATGCT--	GATTAGTGGCGCA	: 104
Hcholescys :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 88
Hpamatensi :	CTCTCTAGCTTGCTAG	GAGTG--		GATTAGTGGCGCA	: 108
Hmustelae :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 107
Hrodentium :	C--TCTAGCTTGCTAG	GTGG----		GATTAGTGGCGCA	: 82
Hpullorum :	C--TCTAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 99
Hfennellia :	TC--C-TAGCTTGCTAG	GATG----		GATTAGTGGCGCA	: 107
Htrogontum :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 84
Hmuridarum :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 104
Hhepaticus :	CTTC-TAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 83
Abutzleri :	GATTATAGCTTGCTAT	ATTGTCACT		GATTAGTGGCGCA	: 108
Cjejuni gb :	C--TCTAGCTTGCTAG	AGTG--		GATTAGTGGCGCA	: 105
Wsuccinoge :	GGGTGTAGCTTGCTAT	CTGCT--		GATTAGTGGCGCA	: 108
	c	tagCTTGctag		gattAGTGGCGCA	

Figure 2 - 3

	120	*	140	
Hsuis2BXA0 :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 85
Ghominis1 :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 112
Ghominis2 :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 113
Hfelis gb :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 140
Hbizzozero :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 113
Hbilis gb :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 135
Hsalomonis :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 70
Hpylori gb :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 145
Hcanis gb :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 135
Hcinaedi g :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 143
Hacinonych :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 144
Hnemestrin :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 141
Hcholescys :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 125
Hpamatensi :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 145
Hmustelae :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 144
Hrodentium :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 119
Hpullorum :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 136
Hfennellia :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 144
Htrogontum :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 121
Hmuridarum :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 141
Hhepaticus :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 120
Abutzleri :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 145
Cjejuni gb :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 142
Wsuccinoge :	CGGGTGAGTAA	GCATAGATG	CATGCCC	TTAGTTT : 145

CGGGTGAGTAA GcATAG T A TGCCc ttAgt t

Figure 2 - 4

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	*	160	*	180		
Hsuis2BXA0 :	GG	AATAGCCA	TAGAAAT	GGTGATTAAATAC	AAATAC : 122	
Ghominis1 :	GG	AATAGCCA	TAGAAAT	GGTGATTAAATAC	AAATAC : 149	
Ghominis2 :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	AAATAT : 150	
Hfelis gb :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	AAATAC : 177	
Hbizzozero :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	AAATAC : 150	
Hbilis gb :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 172	
Hsalomonis :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	AAATAC : 107	
Hpylori gb :	GGG	ATAGCCATT	GAAA	GATGATTAAATAC	AAATAC : 182	
Hcanis gb :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 172	
Hcinaedi g :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 180	
Hacinonych :	GGG	ATAGCCATT	GAAA	GGTGATTAAATAC	AAATAT : 181	
Hnemestrin :	GGG	ATAGCCATT	GAAA	GATAGATTAAATAC	AAATAC : 178	
Hcholescys :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 162	
Hpamatensi :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 182	
Hmustelae :	GGG	ATAGCCATT	GAAA	GGTGATTAAATAC	TGATAC : 181	
Hrodentium :	AGG	ATAGCCATT	GAAA	GATGATTAAATAC	TGATAC : 156	
Hpullorum :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 173	
Hfennellia :	AGG	ATANNNN	NNN	GAAA	GGTGATTAAATAC	NNNNNN : 181
Htrogontum :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 158	
Hmuridarum :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 178	
Hhepaticus :	GGG	ATAGCCA	TAGAAAT	GGTGATTAAATAC	TGATAC : 157	
Abutzleri :	GGG	ATACAAATT	GAAA	GATTGCTAATAC	TTATAT : 182	
Cjejuni gb :	AGG	ACACAGTT	GAAA	CACTGCTNATACT	TCTATAC : 179	
Wsuccinoge :	GG	AATAGCCAGT	GAAA	GGTGATTAAATAC	GGATAT : 182	
		gGgAtAgCca	T	GAAA	GgtgatTAATAC	ATAC

Figure 2 - 5

	*	200	*	220	
Hsuis2BXA0 :	TAGCTT	-----	ATGAGGGGAAGA	TTT	: 143
Ghominis1 :	TAGCTT	-----	ATGAGGGGAAGA	TTT	: 170
Ghominis2 :	TAGCCT	-----	ATGGGGGAAGA	TTT	: 171
Hfelis gb :	T--CCT	-----	ATGGGGGAAGA	TTT	: 196
Hbizzozero :	TAGCCT	-----	ATGGGGGAAGA	TTT	: 171
Hbilis gb :	TCCT	-----	ATGGGGGAAGGGGC	TTT	: 195
Hsalomonis :	TAGCCT	-----	ATGGGGGAAGA	TTT	: 128
Hpylori gb :	T--CCT	-----	ATGGGGGAAGA	TTT	: 201
Hcanis gb :	TCCT	-----	ATGGGGGAAG	TTT	: 191
Hcinaedilg :	TCCT	-----	ATGGGGGAAGG	TTT	: 199
Hacinonych :	T--CCT	-----	ATGGGGGAAGA	TTT	: 200
Hnemestrin :	T--CCT	-----	ATGGGGGAAGA	TTT	: 197
Hcholescys :	T--CCC	-----	TACGGGGGAAG	TTT	: 181
Hpamatensi :	T--CCT	-----	TACGAGGGGAAG	TTT	: 201
Hmustelae :	T--CCT	-----	ATGGGGGAAG	NTN	: 200
Hrodentium :	TCCT	-----	ATGGGGGAAG	TTT	: 175
Hpullorum :	TCCT	-----	ATGGGGGAAG	TTT	: 192
Hfennellia :	N--NNN	-----	NNNNNNNNNN	NNC	: 200
Htrogontum :	TCCTT	-----	ATGAGGGGAAG	TTT	: 177
Hmuridarum :	TCCT	-----T-----	ATGGGGGAAG	TTT	: 196
Hhepaticus :	TCCT	-----	ATGGGGGAAG	TTT	: 176
Abutzleril :	TCCTTTTATCAAAAGATA	AAAAGGGGAAGA	TTT	: 216	
Cjejuni gb :	TCCTGCTTAACACAAGTTG	AGTAGGGGAAG	TNT	: 212	
Wsuccinoge :	TCCTG	-----	AGAGGGGAAG	TTT	: 201

T c a gggGGaAAG Ttt

Figure 2 - 6

	*	240	*	26	
Hsuis2BXA0	:	-----	:		-
Ghominis1	:	-----	:		-
Ghominis2	:	-----	:		-
Hfelis gb	:	-----	:		-
Hbizzozero	:	-----	:		-
Hbilis gb	:	CAATAAAGAATTTCTCTTTT	:	AGTGCTTTGTGTTGTT	232
Hsalomonis	:	-----	:		-
Hpylori gb	:	-----	:		-
Hcanis gb	:	-----	:		-
Hcinaedi g	:	-----	:		-
Hacinonych	:	-----	:		-
Hnemestrin	:	-----	:		-
Hcholescys	:	-----	:		-
Hpamatensi	:	-----	:		-
Hmustelae	:	-----	:		-
Hrodentium	:	-----	:		-
Hpullorum	:	-----	:		-
Hfennellia	:	-----	:		-
Htrogontum	:	-----	:		-
Hmuridarum	:	-----	:		-
Hhepaticus	:	-----	:		-
Abutzleri	:	-----	:		-
Cjejuni gb	:	-----	:		-
Wsuccinoge	:	-----	:		-

Figure 2 - 7

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	0	*	280	*	
Hsuis2BXA0	:	-----	:		-
Ghominis1	:	-----	:		-
Ghominis2	:	-----	:		-
Hfelis gb	:	-----	:		-
Hbizzozero	:	-----	:		-
Hbilis gb	:	GGCACAAAATTCTAGTATTTGGAATGAGAAATTGATG	:	269	-
Hsalomonis	:	-----	:		-
Hpylori gb	:	-----	:		-
Hcanis gb	:	-----	:		-
Hcinaedi g	:	-----	:		-
Hacinonych	:	-----	:		-
Hnemestrin	:	-----	:		-
Hcholescys	:	-----	:		-
Hpamatensi	:	-----	:		-
Hmustelae	:	-----	:		-
Hrodentium	:	-----	:		-
Hpullorum	:	-----	:		-
Hfennellia	:	-----	:		-
Htrogontum	:	-----	:		-
Hmuridarum	:	-----	:		-
Hhepaticus	:	-----	:		-
Abutzleri	:	-----	:		-
Cjejuni gb	:	-----	:		-
Wsuccinoge	:	-----	:		-

Figure 2 - 8

	300	*	320	*	
Hsuis2BXA0	:	-----	:		-
Ghominis1	:	-----	:		-
Ghominis2	:	-----	:		-
Hfelis gb	:	-----	:		-
Hbizzozero	:	-----	:		-
Hbilis gb	:	TTGTGAAGCAATTTGTGCGGAGACTAGACTTAGTGTC	:		306
Hsalomonis	:	-----	:		-
Hpylori gb	:	-----	:		-
Hcanis gb	:	-----	:		-
Hcinaedi g	:	-----	:		-
Hacinonych	:	-----	:		-
Hnemestrin	:	-----	:		-
Hcholescys	:	-----	:		-
Hpamatensi	:	-----	:		-
Hmustelae	:	-----	:		-
Hrodentium	:	-----	:		-
Hpullorum	:	-----	:		-
Hfennellia	:	-----	:		-
Htrogontum	:	-----	:		-
Hmuridarum	:	-----	:		-
Hhepaticus	:	-----	:		-
Abutzleri	:	-----	:		-
Cjejuni gb	:	-----	:		-
Wsuccinoge	:	-----	:		-

Figure 2 - 9

	340	*	360	*	
Hsuis2BXAO :	-----		-----		-
Ghominis1l :	-----		-----		-
Ghominis2l :	-----		-----		-
Hfelis gbl :	-----		-----		-
Hbizzozero :	-----		-----		-
Hbilis gbl :	TGTCGCACAAGCAAATTGCGAACTCATCGATTATCG				343
Hsalomonis :	-----		-----		-
Hpylori gb :	-----		-----		-
Hcanis gbl :	-----		-----		-
Hcinaedi g :	-----		-----		-
Hacinonych :	-----		-----		-
Hnemestrin :	-----		-----		-
Hcholescys :	-----		-----		-
Hpamatensi :	-----		-----		-
Hmustelae :	-----		-----		-
Hrodentium :	-----		-----		-
Hpullorum :	-----		-----		-
Hfennellia :	-----		-----		-
Htrogontum :	-----		-----		-
Hmuridarum :	-----		-----		-
Hhepaticus :	-----		-----		-
Abutzleri :	-----		-----		-
Cjejuni gb :	-----		-----		-
Wsuccinoge :	-----		-----		-

Figure 2 - 10

	380	*	400	
Hsuis2BXA0 :	-----AT-----		CGCTA	: 152
Ghominis1 :	-----AT-----		CGCTA	: 179
Ghominis2 :	-----AT-----		CGCTA	: 180
Hfelis gb :	-----AT-----		CGCTA	: 205
Hbizzozero :	-----AT-----		CGCTA	: 180
Hbilis gb :	TCCAAAGACGAATTTT	TATTGAAAGCCTT	CGCTA	: 380
Hsalomonis :	-----AT-----		CGCTA	: 137
Hpylori gb :	-----AT-----		CGCTA G	: 210
Hcanis gb :	-----T-----	T-----	CGCTA	: 200
Hcinaedi g :	-----T-----	T-----	CGCTA	: 208
Hacinonych :	-----AT-----		CGCTA G	: 209
Hnemestrin :	-----AT-----		CGCTA G	: 206
Hcholescys :	-----TT-----		CGCTA	: 190
Hpamatensi :	-----TT-----		CGCTATG	: 210
Hmustelael :	-----TT-----		CGCTATG	: 209
Hrodentium :	-----TT-----		CGCTA	: 184
Hpullorum :	-----TT-----		CGCTA G	: 201
Hfennellia :	-----TC-----		CGCTA	: 209
Htrogontum :	-----TT-----		CGCTATG	: 186
Hmuridarum :	-----TT-----		CGCTA	: 205
Hhepaticus :	-----TT-----		CGCTA	: 185
Abutzleri :	-----NT-----		TGGTA G	: 225
Cjejuni gb :	-----TT-----		CGGTGT	: 221
Wsuccinoge :	-----TT-----		CGCTATG	: 210
	t		cGcTa	

Figure 2 - 11

```

      *      420      *      440
Hsuis2BXA0 : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 189
Ghominis1| : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 216
Ghominis2| : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 217
Hfelis|gb| : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 242
Hbizzozero : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 217
Hbilis|gb| : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 417
Hsalomonis : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 174
Hpylori|gb| : AGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 247
Hcanis|gb| : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 237
Hcinaedilg : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 245
Hacinonych : AGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 246
Hnemestrin : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 243
Hcholescys : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 227
Hpamatensi : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 247
Hmustelae| : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 246
Hrodentium : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 221
Hpullorum| : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 238
Hfennellia : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 246
Htrogontum : GGATTGGTCTATGTCCTATCAGCTTGTGGTGAGGTA : 223
Hmuridarum : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 242
Hhepaticus : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 222
Abutzler| : AGATTGGCTGTAATTGATCAGTTAGTTGGTGAGGTA : 262
Cjejuni|gb| : GGATGAGACTATATAGFATCAGCTAGTTGGTGAGGTA : 258
Wsuccinoge : GGATCGGCTATGTCCTATCAGCTTGTGGTGAGGTA : 247
gGAT G CTaTgtccTATCAGcTtGTTGGTgaGGTA

```

Figure 2 - 12

	*	460	*	480	
Hsuis2BXA0	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	226
Ghominis1	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	253
Ghominis2	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	254
Hfelis gb	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	279
Hbizzozero	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	254
Hbilis gb	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	454
Hsalomonis	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	211
Hpylori gb	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	284
Hcanis gb	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	274
Hcinaedilg	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	282
Hacinonych	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	283
Hnemestrin	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	280
Hcholescys	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	264
Hpamatensi	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	284
Hmustelae	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	283
Hrodentium	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	258
Hpullorum	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	275
Hfennellia	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	283
Htrogontum	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	260
Hmuridarum	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	279
Hhepaticus	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	259
Abutzleri	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	299
Cjejuni gb	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	295
Wsuccinoge	:	AAGGCTCACC	AAGGCTATGACGGGTATCCGGCCTGAG	:	284

A gGCTcACCAAGgCtATGACGggTAtCcGGccTGAG

Figure 2 - 13

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	*	500	*	5	
Hsuis2BXA0 :	AGGGTGAGCGGACACACTGGAACTGAGACACGGTCCA				: 263
Ghominis1 :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 290
Ghominis2 :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 291
Hfelis gb :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 316
Hbizzozero :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 291
Hbilis gb :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 491
Hsalomonis :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 248
Hpylori gb :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 321
Hcanis gb :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 311
Hcinaedi g :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 319
Hacinonych :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 320
Hnemestrin :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 317
Hcholescys :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 301
Hpamatensi :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 321
Hmustelae :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 320
Hrodentium :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 295
Hpullorum :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 312
Hfennellia :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 320
Htrogonum :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 297
Hmuridarum :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 316
Hhepaticus :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 296
Abutzleri :	AGGATGATCAGTCACACTGGAAGTGAACACCGGTCCA				: 336
Cjejuni gb :	AGGATGATCAGTCACACTGGAAGTGAACACCGGTCCA				: 332
Wsuccinoge :	AGGGTGACCGGACACACTGGAAGTGAACACCGGTCCA				: 321

AGGgTGA CgGaCACACTGGAAGTGAACACCGGTCCA

Figure 2 - 14

	20	*	540	*	
Hsuis2BXA0 :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	300	
Ghominis1 :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	327	
Ghominis2 :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	328	
Hfelis gb :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	353	
Hbizzozero :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	328	
Hbilis gb :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	528	
Hsalomonis :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	285	
Hpylori gb :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	358	
Hcanis gb :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	348	
Hcinaedilg :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	356	
Hacinonych :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	357	
Hnemestrin :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	354	
Hcholescys :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	338	
Hpmatensi :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	358	
Hmustelae :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	357	
Hrodentium :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	332	
Hpullorum :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	349	
Hfennellia :	GNCTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	357	
Htrogontum :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	334	
Hmuridarum :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	353	
Hhepaticus :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	333	
Abutzleri :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	373	
Cjejuni gb :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	369	
Wsuccinoge :	GACTCCTACGGGAGGCAGCAGT	AGGGGAATATTGCTCA	:	358	
	GACTCCTACGGGAGGCAGCAGTaGGGAATATTGCTCA				

Figure 2 - 15

	560	*	580	*	
Hsuis2BXA0	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	337	
Ghominis1	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	364	
Ghominis2	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	365	
Hfelis gb	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	390	
Hbizzozero	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	365	
Hbilis gb	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	565	
Hsalomonis	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	322	
Hpylori gb	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	395	
Hcanis gb	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	385	
Hcinaedi g	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	393	
Hacinonych	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	394	
Hnemestrin	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	391	
Hcholescys	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	375	
Hpamatensi	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	395	
Hmustelael	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	394	
Hrodentium	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	369	
Hpullorum	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	386	
Hfennellia	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	394	
Htrogontum	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	371	
Hmuridarum	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	390	
Hhepaticus	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	370	
Abutzleri	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	410	
Cjejuni gb	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	406	
Wsuccinoge	: ATGGGGGAAAC	CCTGAAGCAGCAACGCCGCGTGGAGG	:	395	
	ATGGG	GaAA	ccTGAaGCAGCAACGCCGCGTGGAGG		

Figure 2 - 16

	600	*	620	
Hsuis2BXA0 :	ATGAAGGTTT	TAGGATCGTAAACTCCTTTT	TTAGAG	: 374
Ghominis1 :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 401
Ghominis2 :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 402
Hfelis gb :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 427
Hbizzozero :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 402
Hbilis gb :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 602
Hsalomonis :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 359
Hpylori gb :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 432
Hcanis gb :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 422
Hcinaedi g :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 430
Hacinonych :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 431
Hnemestrin :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 428
Hcholescys :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 412
Hpamatensi :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 432
Hmustelae :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 431
Hrodentium :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 406
Hpullorum :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 423
Hfennellia :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 431
Htrogontum :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 408
Hmuridarum :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 427
Hhepaticus :	ATGAAGGTTT	TAGGATTGTAAACTCCTTTT	TTAGAG	: 407
Abutzleri :	ATGACACATT	TCGGTGCCTAAACTCCTTTT	ATATAAG	: 447
Cjejuni gb :	ATGACACTTT	TCGGAGCCTAAACTCCNNTT	CTAGGG	: 443
Wsuccinoge :	ATGAAGGTCT	TCGGATTGTAAACTCCTTTT	CTAAGAG	: 432

ATGAaggtttTaGGattGTAAACTCCTTTT T agaG

Figure 2 -17

	*	640	*	660	
Hsuis2BXA0 :	AAGA-	TAATGACGGTATCTAA	GAATAAGCACCGGCT	:	410
Ghominis1 :	AAGA-	TAATGACGGTATCTAA	GAATAAGCACCGGCT	:	437
Ghominis2 :	AAGA-	TAATGACGGTATCTCA	GAATAAGCACCGGCT	:	438
Hfelis gb :	AAGA-	TAATGACGGTATCTGA	GAATAAGCACCGGCT	:	463
Hbizzozero :	AAGA-	TAATGACGGTATCTGA	GAATAAGCACCGGCT	:	437
Hbilis gb :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	638
Hsalomonis :	AAGA-	TAATGACGGTATCTCA	GAATAAGCACCGGCT	:	395
Hpylori gb :	AAGA-	TAATGACGGTATCTAA	GAATAAGCACCGGCT	:	468
Hcanis gb :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	458
Hcinaedi g :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	466
Hacinonych :	AAGA-	TAATGACGGTATCTGA	GAATAAGCACCGGCT	:	467
Hnemestrin :	AAGA-	TAATGACGGTATCTAA	GAATAAGCACCGGCT	:	464
Hcholescys :	AAGA-	TTATGACGGTATCTCA	GAATAAGCACCGGCT	:	448
Hpamatensi :	AAGA-	TTATGACGGTATCTAA	GAATAAGCACCGGCT	:	468
Hmustelae :	AAGA-	TAATGACGGTATCTTA	GAATAAGCACCGGCT	:	467
Hrodentium :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	442
Hpullorum :	AAGA-	TAATGACGGTATCTAA	GAATAAGCACCGGCT	:	459
Hfennellia :	AAGA-	TTATGACGGTATCTAA	GAATAAGCACCGGCT	:	467
Htrogonum :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	444
Hmuridarum :	AAGA-	TTATGACGGTATCTCA	GAATAAGCACCGGCT	:	463
Hhepaticus :	AAGA-	TTATGACGGTATCTAA	GAATAAGCACCGGCT	:	443
Abutzleri :	AAGA-	TAATGACGGTATCTAT	GAATAAGCACCGGCT	:	483
Cjejuni gb :	AAGAATTCTG	ACGGTACCTAAG	GAATAAGCACCGGCT	:	480
Wsuccinoge :	AAGA-	TTATGACGGTATCTTA	GAATAAGCACCGGCT	:	468
	AAGA	T	aTGACGGTAtct	A	GAaTAAGCACCGGCT

Figure 2 - 18

	*	680	*	700	
Hsuis2BXA0 :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	447	
Ghominis1 :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	474	
Ghominis2 :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	475	
Hfelis gb :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	500	
Hbizzozero :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	474	
Hbilis gb :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	675	
Hsalomonis :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	432	
Hpylori gb :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	505	
Hcanis gb :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	495	
Hcinaedilg :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	503	
Hacinonych :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	504	
Hnemestrin :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	501	
Hcholescys :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	485	
Hpamatensi :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	505	
Hmustelae :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	504	
Hrodentium :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	479	
Hpullorum :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	496	
Hfennellia :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	504	
Htrogonum :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	481	
Hmuridarum :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	500	
Hhepaticus :	AACTCCGTGCC	-----CGGAGGGTGC	:	464	
Abutzleri :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	520	
Cjejuni gb :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	517	
Wsuccinoge :	AACTCCGTGCCAGCAGCCGCGGTAATA	CGGAGGGTGC	:	505	
	AACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGC				

Figure 2 - 19

	*	720	*	740	
Hsuis2BXA0 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 484
Ghominis1 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 511
Ghominis2 :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 512
Hfelis gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 537
Hbizzozero :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 511
Hbilis gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 712
Hsalomonis :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 469
Hpylori gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 542
Hcanis gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 532
Hcinaedi g :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 540
Hacinonych :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 541
Hnemestrin :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 538
Hcholescys :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 522
Hpamatensi :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 542
Hmustelae :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 541
Hrodentium :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 516
Hpullorum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 533
Hfennellia :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 541
Htrogontum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 518
Hmuridarum :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 537
Hhepaticus :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 501
Abutzleri :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 557
Cjejuni gb :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 554
Wsuccinoge :	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTGCCT				: 542
	AAGCGTTACTCGGAATCACTGGGCGTAAAGAGTgcGt				

Figure 2 -20

* 760 *

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Hsuis2BXA0 : AGGCGGGAGGACAAGTCAGGTGTGAAATCCTTTGCT : 521
Ghominis1| : AGGCGGGAGGACAAGTCAGGTGTGAAATCCTTTGCT : 548
Ghominis2| : AGGCGGGGTTCAAGTCAGGTGTGAAATCCTTTGCT : 549
Hfelis|gb| : AGGCGGGGTTCAAGTCAGGTGTGAAATCCTTTGCT : 574
Hbizzozero : AGGCGGGGTTCAAGTCAGGTGTGAAATCCTTTGCT : 548
Hbilis|gb| : AGGCGGGAGTCAAGTCAGGTGTGAAATCCTTTAGCT : 749
Hsalomonis : AGGCGGGGTTCAAGTCAGGTGTGAAATCCTTTGCT : 506
Hpylori|gb : AGGCGGGATTCAGTCAGGTGTGAAATCCTTTGCT : 579
Hcanis|gb| : AGGCGGGAAGTCAAGTCAGGTGTGAAATCCTTTAGCT : 569
Hcinaedi|g : AGGCGGGTAGTCAAGTCAGGTGTGAAATCCTTTAGCT : 577
Hacinonych : AGGCGGGRTTCAAGTCAGGTGTGAAATCCTTTGCT : 578
Hnemestrin : AGGCGGGATTCAGTCAGGTGTGAAATCCTTTGCT : 575
Hcholescys : AGGCGGGGTCAAGTCAGGTGTGAAATCCTTTGCT : 559
Hpamatensi : AGGCGGGGTCAAGTCAGGTGTGAAATCCTTTGCT : 579
Hmustelae| : AGGCGGGAGTCAAGTCAGGTGTGAAATCCTTTAGCT : 578
Hrodentium : AGGCGGGATTCAGTCAGGTGTGAAATCCTTTGCT : 553
Hpullorum| : AGGCGGGGTCAAGTCAGGTGTGAAATCCTTTGCT : 570
Hfennellia : AGGCGGGATTCAGTCAGGTGTGAAATGCTTTGCT : 578
Htrogontum : AGGCGGGGTCAAGTCAGGTGTGAAATCCTTTAGCT : 555
Hmuridarum : AGGCGGGCTCAAGTCAGGTGTGAAATCCTTTAGCT : 574
Hhepaticus : AGGCGGGGTCAAGTCAGGTGTGAAATCCTTTAGCT : 538
Abutzleri| : AGGCGGATTCAAGTCTTCAAGTGAATCCTTTAGCT : 594
Cjejuni|gb : AGGCGGATTCAAGTCTTCAAGTGAATCTATTTGCT : 591
Wsuccinoge : AGGCGGCCTTCAAGTCAGGTGTGAAATCCAATGCT : 579
AGGCGGg t aAGTcag tGTGAAATcct t GCT

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Figure 2 -21

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780          *          800          *
Hsuis2BXAO : TAAC A AGAACTGCATTGAAACT TCCTTCTGGAG : 558
Ghominis1| : TAAC A AGAACTGCATTGAAACT TCTTCTGGAG : 585
Ghominis2| : TAAC A AGAACTGCATTGAAACT GAACCTTGGAG : 586
Hfelis|gb| : TAAC A AGAACTGCATTGAAACT TAACTCTGGAG : 611
Hbizzozero : TAAC A AGAACTGCATTGAAACT TAACTCTGGAG : 585
Hbilis|gb| : TAACTACAGAACTGCATTGAAACT TTTTCTGGAG : 786
Hsalomonis : TAAC A AGAACTGCATTGAAACT TAACTCTGGAG : 543
Hpylori|gb| : TAAC A AGAACTGCATTGAAACT TTTTCTGGAG : 616
Hcanis|gb| : TAACTACAGAACTGCATTGAAACT TTTTCTGGAG : 606
Hcinaedi|g : TAACTACAGAACTGCATTGAAACT GACTATCTGGAG : 614
Hacinonych : TNACCAAGAACTGCATTGAAACT TAYTCTGGAG : 615
Hnemestrin : TAAC A AGAACTGCATTGAAACT TTTTCTGGAG : 612
Hcholescys : TAAC A AGAACTGCATTGAAACT TAACTCTGGAG : 596
Hpamateni : TAAC A AGAACTGCATTGAAACT TAACTCTGGAG : 616
Hmustelae| : TAACTACAGAACTGCATTGAAACT GTTTTCTGGAG : 615
Hrodentium : TAAC A AGAACTGCATTGAAACT GTTTTCTGGAG : 590
Hpullorum| : TAAC A AGAACTGCATTGAAACT TAACTCTGGAG : 607
Hfennellia : TAAC A AGAACTGCATTGAAACT GTTTTCTGGAG : 615
Htrogontum : TAACTACAGAACTGCATTGAAACT GTTTTCTGGAG : 592
Hmuridarum : TAACTAAGAACTGCATTGAAACT TTTTCTGGAG : 611
Hhepaticus : TAACTACAGAACTGCATTGAAACT GTTTTCTGGAG : 575
Abutzleri| : TAACTAAGAACTGCTTTGAAACTGT TAACTCTGGA : 631
Cjejuni|gb| : TAACCA TAACTGCTTTGGAAACTGATGTCNAGAG : 628
Wsuccinoge : TAACGGTGAAGCTGCATTGAAACTGAAGGCNAGAG : 616
TAAC a agAACTGCaTttgAAACT a tCT GAg

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Figure 2 - 22

	820	*	840	*	
Hsuis2BXA0 :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGCTA	:	595	
Ghominis1 :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	622	
Ghominis2 :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	623	
Hfelis gb :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	648	
Hbizzozero :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	622	
Hbilis gb :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	823	
Hsalomonis :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	580	
Hpylori gb :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	653	
Hcanis gb :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	643	
Hcinaedi g :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	651	
Hacinonych :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	652	
Hnemestrin :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	649	
Hcholescys :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	633	
Hpamatsensi :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	653	
Hmustelae :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	652	
Hrodentium :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	627	
Hpullorum :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	644	
Hfennellia :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	652	
Htrogontum :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	629	
Hmuridarum :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	648	
Hhepaticus :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	612	
Abutzleri :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	668	
Cjejuni gb :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	665	
Wsuccinoge :	T	TGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA	:	653	
	T	tGGGAGAGGTAGGTGGAATTCTTGGTGTAGGGGTA			

Figure 2 - 23

	860	*	880	
Hsuis2BXA0	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	632	
Ghominis1	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	659	
Ghominis2	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	660	
Hfelis gb	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	685	
Hbizzozero	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	659	
Hbilis gb	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	860	
Hsalomonis	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	617	
Hpylori gb	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	690	
Hcanis gb	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	680	
Hcinaedi g	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	688	
Hacinonych	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	689	
Hnemestrin	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	686	
Hcholescys	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	670	
Hpamatensi	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	690	
Hmustelae	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	689	
Hrodentium	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	664	
Hpullorum	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	681	
Hfennellia	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	689	
Htrogontum	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	666	
Hmuridarum	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	685	
Hhepaticus	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	649	
Abutzler	: AAATCCGTAGAGATCAAGAGGAATACTCATTGCCGAAG	:	705	
Cjejuni gb	: AAATCCGTAGATATCACCAGAATACCCATTGCCGAAG	:	702	
Wsuccinoge	: AAATCCGTAGAGATCGAGAGGAATACTCATTGCCGAAG	:	690	
	AAATCCGTAGAGATCaagAgGAATACTcATTGCCGAAG			

Figure 2 - 24

	*	900	*	920	
Hsuis2BXA0	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 669
Ghominis1	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 696
Ghominis2	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 697
Hfelis gb	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 721
Hbizzozero	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 696
Hbilis gb	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 896
Hsalomonis	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 654
Hpylori gb	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 727
Hcanis gb	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 716
Hcinaedi g	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 724
Hacinonych	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 726
Hnemestrin	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 723
Hcholescys	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 706
Hpamatensi	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 726
Hmustelae	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 725
Hrodentium	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 700
Hpullorum	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 717
Hfennellia	:	GNGACCTACTGGAACA	TACTGACGCTGAT	TGCACGA	: 725
Htrogontum	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 702
Hmuridarum	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 721
Hhepaticus	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 685
Abutzlerii	:	GCGATCTACTGGAACA	CACTGACGCTGAT	TGCACGA	: 741
Cjejuni gb	:	GCGATCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 738
Wsuccinoge	:	GCGACCTGCTGGAACA	CACTGACGCTGAT	TGCACGA	: 726
		GCGAcCTgCTGGAACa	tAcTGACGCTgAt	gc CgA	

Figure 2 - 25

	*	940	*	960	
Hsuis2BXA0 :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 706
Ghominis1 :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 733
Ghominis2 :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 734
Hfelis gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 758
Hbizzozero :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 733
Hbilis gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 933
Hsalomonis :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 691
Hpylori gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 764
Hcanis gb :	AAGC-TGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 752
Hcinaedi g :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 761
Hacinonych :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 763
Hnemestrin :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 760
Hcholescys :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 743
Hpamatensi :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 763
Hmustelae :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 762
Hrodentium :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 737
Hpullorum :	AAGC-TGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 753
Hfennellia :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 762
Htrogontum :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 739
Hmuridarum :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 758
Hhepaticus :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 722
Abutzleri :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 778
Cjejuni gb :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 775
Wsuccinoge :	AAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG				: 763
	AAGCgTGGGGAGCAAACAGGATTAGATACCCTGGTAG				

Figure 2 - 26

	*	980	*	100	
Hsuis2BXA0 :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	GGGAGG	:	743
Ghominis1 :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	G-AGG	:	769
Ghominis2 :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	GGGGG	:	771
Hfelis gb :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	GGGGG	:	795
Hbizzozero :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	GGGGG	:	770
Hbilis gb :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	CCCTG	:	970
Hsalomonis :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	GGGGG	:	728
Hpylori gb :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	GAGGG	:	801
Hcanis gb :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	CCCTG	:	789
Hcinaedil g :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	CCCTG	:	798
Hacinonych :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	GRRGG	:	800
Hnemestrin :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	GAGGG	:	797
Hcholescys :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	GGGGT	:	780
Hpamatensi :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	TGGAG	:	800
Hmustelae :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	GGGGT	:	799
Hrodentium :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	CGAGG	:	774
Hpullorum :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	TGAGG	:	790
Hfennellia :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	CCCTG	:	799
Htrogontum :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	CCCTG	:	776
Hmuridarum :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	CCCTG	:	795
Hhepaticus :	TCCACGCCCTAAACGATG	GATGCTAGTTGTTG	CCCTG	:	759
Abutzleri :	TCCACGCCCTAAACGATG	TACACTAGTTGTTG	TGAGG	:	815
Cjejuni gb :	TCCACGCCCTAAACGATG	TACACTAGTTGTTG	GGGGT	:	812
Wsuccinoge :	TCCACGCCCTAAACGATG	CAATGCTAGTTGTTG	CCCTG	:	800
	TCCACGCCCTAAACGATG	AtgCTAGTTGTTG	G		

Figure 2 - 27

	0	*	1020	*	
Hsuis2BXA0 :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 780
Ghominis1 :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 806
Ghominis2 :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 808
Hfelis gb :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 831
Hbizzozero :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 807
Hbilis gb :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 1006
Hsalomonis :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 765
Hpylori gb :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 838
Hcanis gb :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 825
Hcinaedi g :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 834
Hacinonych :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 837
Hnemestrin :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 834
Hcholescys :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 816
Hpamatensi :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 836
Hmustelae :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 835
Hrodentium :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 810
Hpullorum :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 826
Hfennellia :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 835
Htrogontum :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 812
Hmuridarum :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 831
Hhepaticus :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 795
Abutzleril :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGTG	: 851
Cjejuni gb :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGTG	: 848
Wsuccinoge :	CTT	TGTC	TTTCCAGTAATGCAGCTAACGGC	TTAAGCA	: 836
	CTT	GtC	CAGTAATGCAGCTAACGc	TTAAGca	

Figure 2 - 28

	1040	*	1060	*	
Hsuis2BXA0 :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	817	
Ghominis1 :	TCC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	842	
Ghominis2 :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	845	
Hfelis gb :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	868	
Hbizzozero :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	844	
Hbilis gb :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	1043	
Hsalomonis :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	802	
Hpylori gb :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	875	
Hcanis gb :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	862	
Hcinaedi g :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	871	
Hacinonych :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	874	
Hnemestrin :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	871	
Hcholescys :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	853	
Hpamatensi :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	873	
Hmustelae :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	872	
Hrodentium :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	847	
Hpullorum :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	863	
Hfennellia :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	872	
Htrogontum :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	849	
Hmuridarum :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	868	
Hhepaticus :	TC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	832	
Abutzleri :	TAC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	888	
Cjejuni gb :	TAC	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	885	
Wsuccinoge :	TT	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA	:	873	
	T	CGCCTGGGGAGTACGGTCGCAAGATTAAAACTCA			

Figure 2 - 29

	1080	*	1100	*	
Hsuis2BXA0 :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				854
Ghominis1 :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				878
Ghominis2 :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				882
Hfelis gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				905
Hbizzozero :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				881
Hbilis gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				1080
Hsalomonis :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				839
Hpylori gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				912
Hcanis gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				899
Hcinaedi g :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				908
Hacinonych :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				911
Hnemestrin :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				908
Hcholescys :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				890
Hpamatensi :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				910
Hmustelae :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				909
Hrodentium :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				884
Hpullorum :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				900
Hfennellia :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				909
Htrogontum :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				886
Hmuridarum :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				905
Hhepaticus :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				869
Abutzleri :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				925
Cjejuni gb :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				922
Wsuccinoge :	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				910
	AAGGAATAGACGGGGACCCGCACAAGCGGTGGAGCAT				

Figure 2 - 30

	1120	*	1140	
Hsuis2BXA0 :	GTGGTTTAAATTCGAAGTTACACGAAGAACCCTTACCTA			: 891
Ghominis1 :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 915
Ghominis2 :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 919
Hfelis gb :	GTGGTTTAAATTCGANNNNNNACGAAGAACCCTTACCTA			: 942
Hbizzozero :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 918
Hbilis gb :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 1117
Hsalomonis :	GTGGTTTAAATTCGATGCTACACGAAGAACCCTTACCTA			: 876
Hpylori gb :	GTGGTTTAAATTCGANNNNACACGAAGAACCCTTACCTA			: 949
Hcanis gb :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 936
Hcinaedi g :	GTGGTTTAAATTCGAGTATACACGAAGAACCCTTACCTA			: 945
Hacinonych :	GTGGTTTAAATTCGANNNNNACGAAGAACCCTTACCTA			: 948
Hnemestrin :	GTGGTTTAAATTCGAAGGTACACGAAGAACCCTTACCTA			: 945
Hcholescys :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 927
Hpamatensi :	GTGGTTTAAATTCGANNNTACACGAAGAACCCTTACCTA			: 947
Hmustelae :	GTGGTTTAAATTCGAKNNNTACACGAAGAACCCTTACCTA			: 946
Hrodentium :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 921
Hpullorum :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 937
Hfennellia :	GTGGTTTAAATTCGAANNNTACACGAAGAACCCTTACCTA			: 946
Htrogontum :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 923
Hmuridarum :	GTGGTTTAAATTCGANNNNACACGAAGAACCCTTACCTA			: 942
Hhepaticus :	GTGGTTTAAATTCGAAGATACACGAAGAACCCTTACCTA			: 906
Abutzleri :	GTGGTTTAAATTCGANNNNACACGAAGAACCCTTACCTG			: 962
Cjejuni gb :	GTGGTTTAAATTCGAAGNTACACGAAGAACCCTTACCTG			: 959
Wsuccinoge :	GTGGTTTAAATTCGANNNNACACGAAGAACCCTTACCTG			: 947
	GTGGTTTAAATTCGAagaTAC CGAAGAACCCTTACCTa			

Figure 2 -31

	*	1160	*	1180	
Hsuis2BXA0 :	GGCTTGACATTGAAGGAATTC	CTAGAAATAGGGGAG	:	928	
Ghominis1 :	GGCTTGACATTGAAGGAATTC	CTAGAAATAGGGGAG	:	952	
Ghominis2 :	GGCTTGACATTGAAGGAATTC	CTAGAAATAGGGGAG	:	956	
Hfelis gb :	GGCTTGACATTGAAGGAATTC	CTAGAAATAGGGGAG	:	979	
Hbizzozero :	GGCTTGACATTGAAGGAATTC	CTAGAAATAGGGGAG	:	955	
Hbilis gb :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	1154	
Hsalomonis :	GGCTTGACATTGAAGGAATTC	CTAGAAATAGGGGAG	:	913	
Hpylori gb :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	986	
Hcanis gb :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	973	
Hcinaedi g :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	982	
Hacinonych :	GGCTTGACATTGAAGGAATTC	CTAGAAATAGGGGAG	:	985	
Hnemestrin :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	982	
Hcholescys :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	964	
Hpamatensi :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	984	
Hmustelae :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	983	
Hrodentium :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	958	
Hpullorum :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	974	
Hfennellia :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	983	
Htrogontum :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	960	
Hmuridarum :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	979	
Hhepaticus :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	943	
Abutzleri :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	999	
Cjejuni gb :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	996	
Wsuccinoge :	GGCTTGACATTGATAGAATTC	CTAGAAATAGGGGAG	:	984	

GgCTTGACAttga aGAAtc cTAGA ATAg ggaG

Figure 2 - 32

	*	1200	*	1220	
Hsuis2BXA0 :	TCTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 965
Ghominis1 :	TGTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 989
Ghominis2 :	TGTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 993
Hfelis gb :	TGTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 1016
Hbizzozero :	TGTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 992
Hbilis gb :	TG-CTGGC	TTCCAGAG	CTCTG	AAAAACAGGTGCTGCAC	: 1190
Hsalomonis :	TGTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 950
Hpylori gb :	TGTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 1023
Hcanis gb :	TGTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 1010
Hcinaedi g :	TG-TTGGC	TTCCAGAG	CTCTG	AAAAACAGGTGCTGCAC	: 1018
Hacinonych :	TGTCTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 1022
Hnemestrin :	TGTCTGGC	TTTACAAA	CTCTG	AAAAACAGGTGCTGCAC	: 1019
Hcholescys :	TG-CTGGC	TTCCAGAG	CTCTG	AAAAACAGGTGCTGCAC	: 1000
Hpamatensi :	TG-CTGGC	TTCCAGAG	CTCTG	AAAAACAGGTGCTGCAC	: 1020
Hmustelae :	TGTCTAGT	TTTACAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 1020
Hrodentium :	TG-CTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 994
Hpullorum :	TG-CTGGC	TTCCAGAG	CTCTG	AAAAACAGGTGCTGCAC	: 1010
Hfennellia :	TG-CTGGC	TTCCAGAG	CTCTG	AAAAACAGGTGCTGCAC	: 1019
Htrogontum :	TG---CCCT	TCGGGGAG	CTCTG	AAAAACAGGTGCTGCAC	: 994
Hmuridarum :	TG-CCACT	TTCTGGAG	CTCTG	AAAAACAGGTGCTGCAC	: 1015
Hhepaticus :	TG----CCT	TCGGGGAG	CTCTG	AAAAACAGGTGCTGCAC	: 976
Abutzleri :	TG-TCTG	CTTCCAGAAC	CTCTG	AAAAACAGGTGCTGCAC	: 1035
Cjejuni gb :	TG-CTAGC	TTCCAGAC	CTCTG	AAAAACAGGTGCTGCAC	: 1032
Wsuccinoge :	TG-CCGCT	TTTACGGAG	CTCTG	AAAAACAGGTGCTGCAC	: 1020

TG ct gcTt c agA C TgaAaACAGGTGCTGCAC

Figure 2 - 33

	*	1240	*	12	
Hsuis2BXA0 :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1002
Ghominis1 :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1026
Ghominis2 :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1030
Hfelis gb :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1053
Hbizzozero :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1029
Hbilis gb :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1227
Hsalomonis :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 987
Hpylori gb :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1060
Hcanis gb :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1047
Hcinaedi g :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1055
Hacinonych :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1059
Hnemestrin :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1056
Hcholescys :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1037
Hpamatensi :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1057
Hmustelae :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1057
Hrodentium :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1031
Hpullorum :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1047
Hfennellia :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1056
Htrogontum :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1031
Hmuridarum :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1052
Hhepaticus :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1013
Abutzleri :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1072
Cjejuni gb :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1069
Wsuccinoge :	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				: 1057
	GGCTGTCGTCAGCTCGTGTCTGTCGAGATGTTGGGTTAA				

Figure 2 - 34

```

60          *          1280          *
Hsuis2BXAO : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1039
Ghominis1| : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1063
Ghominis2| : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1067
Hfelis|gb| : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1090
Hbizzozero : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1066
Hbilis|gb| : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1264
Hsalomonis : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1024
Hpylori|gb : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1097
Hcanis|gb| : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1084
Hcinaedi|g : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1092
Hacinonych : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1096
Hnemestrin : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1093
Hcholescys : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1074
Hpamatensi : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1094
Hmustelae| : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1094
Hrodentium : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1068
Hpullorum| : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1084
Hfennellia : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1093
Htrogontum : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1068
Hmuridarum : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1089
Hhepaticus : N----- : 1015
Abutzleri| : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1109
Cjejuni|gb : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1106
Wsuccinoge : GTCCCGCAACGAGCGCAACCCCTTTTCTTAGTTGCTA : 1094
Gtcccgcaacgagcgcaaccctc t cttAGttgcta

```

Figure 2 - 35

```

      1300      *      1320      *
Hsuis2BXA0 : CAGGTTATGCTGCCCACTCTAAGAGACTGCCTGCG : 1076
Ghominis1| : CAGGTTATGCTGCCCACTCTAAGAGACTGCCTGCG : 1100
Ghominis2| : CAGGTGATGCTGAGCTCTCTAAGAGACTGCCTGCG : 1104
Hfelis|gb| : CAGGTAATGCTGAGCTCTCTAAGAGACTGCCTGCG : 1127
Hbizzozero : CAGGTAAAGCTGAGCTCTCTAAGAGACTGCCTGCG : 1103
Hbilis|gb| : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1300
Hsalomonis : CAGGTAATGCTGAGCTCTCTAAGAGACTGCCTGCG : 1061
Hpylori|gb : CAGGTTATGCTGAGCACTCTAAGAGACTGCCTCCG : 1134
Hcanis|gb| : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1120
Hcinaedilg : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1128
Hacinonych : CAGGTAATGCTGAGCACTCTAAGAGACTGCCTCCG : 1133
Hnemestrin : CAGGTAATGCTGAGCACTCTAAGAGACTGCCTCCG : 1129
Hcholescys : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1110
Hpamatensi : CAGTTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1130
Hmustelae| : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1130
Hrodentium : CTATTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1104
Hpullorum| : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1120
Hfennellia : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1129
Htrogontum : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1104
Hmuridarum : GCAGTTATGCTGAGCACTCTAAGAGACTGCCTTCC : 1126
Hhepaticus : -----NNNNNNNNNN----- : 1027
Abutzleri| : CAGTTTATGCTGAGCACTCTAAGAGACTGCCTACC : 1145
Cjejuni|gb : CGGTTATGCCGAGCACTCTAAGATAGACTGCCTTCC : 1142
Wsuccinoge : CGGTTATGCCGAGCACTCTAGTAGACTGCCTTCC : 1130
      cag t      gctgagcaCTCTAag Agactgcct cg

```

Figure 2 - 36

```

1340      *      1360
TAAGCAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1113
TAAN --- AGGAAGGTGAGGACGACGTC AAGTCATCA : 1133
TAAGCANGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1141
TAAACAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1164
TAAGCAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1140
TAAGCAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1337
TAAGCAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1098
TAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1171
TAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1157
TAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1165
TAAGTAGGAGGAAGGTGGGACGACGTC AAGTCATCA : 1170
TAAGTAGGAGGAAGGTGGGACGACGTC AAGTCATCA : 1166
TAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1147
TNAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1167
TNAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1167
CAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1141
TAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1157
CANCTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1166
TAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1141
TAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1163
---NNNNNNNNNNNNNNNNNNNNNNNNNNNN----- : 1053
CAACTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1182
TNAGTAGGAGGAAGGTGGGACGACGTC AAGTCATCA : 1179
CAAGTAGGAGGAAGGTGAGGACGACGTC AAGTCATCA : 1167
taagAaqgAGGAAGGTGaGGAcGACGTCaaqtcatca

```

Figure 2 - 37

	*	1380	*	1400	
Hsuis2BXA0	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1150	
Ghominis1	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1170	
Ghominis2	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1178	
Hfelis gb	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1201	
Hbizzozero	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1177	
Hbilis gb	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1374	
Hsalomonis	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1135	
Hpylori gb	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1208	
Hcanis gb	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1194	
Hcinaedi g	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1202	
Hacinonych	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1207	
Hnemestrin	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1203	
Hcholescys	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1184	
Hpamatensi	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1204	
Hmustelae	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1204	
Hrodentium	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1178	
Hpullorum	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1194	
Hfennellia	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1203	
Htrogontum	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1178	
Hmuridarum	:	TGGCCCTTACGCCTAGGGCTACACACGTGCTACAATG	:	1200	
Hhepaticus	:	-----N-----NNN	:	1057	
Abutzleri	:	TGGCCCTTACGTCCAGGGCTACACACGTGCTACAATG	:	1219	
Cjejuni gb	:	TGGCCCTTATGCCAGGGCGACACACGTGCTACAATG	:	1216	
Wsuccinoge	:	TGGCCCTTACGCCYAGGGCTACACACGTGCTACAATG	:	1204	
		tggcccttAcgcctagggctacacacgtgctacaATG			

Figure 2 - 38


```

      *           1420           *           1440
Hsuis2BXA0 : GGGTGGACAAAGAGATGCAAGAGCGGGAAGCAGAGGT : 1187
Ghominis1| : GGGTGGACAAAGAGATGCAAGAGCGGGAAGCAGAGGT : 1207
Ghominis2| : GGAAGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1215
Hfelis|gb| : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1238
Hbizzozero : GGAAGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1214
Hbilis|gb| : GGACATACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1411
Hsalomonis : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1172
Hpylori|gb : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1245
Hcanis|gb| : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1231
Hcinaedi|g : GGACATACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1239
Hacinonych : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1244
Hnemestrin : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1240
Hcholescys : GTAGGTACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1221
Hpamatensi : GGAAGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1241
Hmustelae| : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1241
Hrodentium : GGAAGTACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1215
Hpullorum| : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1231
Hfennellia : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1240
Htrogontum : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1215
Hmuridarum : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1237
Hhepaticus : NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN : 1094
Abutzleri| : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1256
Cjejuni|gb : GGAAGTACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1253
Wsuccinoge : GGGTGGACAAAGAGATGCAATGCGGGAAGCAGAGGT : 1241
Gg g ACAAagAGa GCaAt c G GA gtgGAGC

```

Figure 2 - 39

Figure 2 -40

Figure 2 - 41

	520	*	1540	*	
Hsuis2BXAO :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1298
Ghominis1 :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1318
Ghominis2 :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1326
Hfelis gb :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1349
Hbizzozero :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1325
Hbilis gb :	TGAATCAGG	AATGT	CACGGTGAATACGTTCCCGGGTC		: 1522
Hsalomonis :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1283
Hpylori gb :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1356
Hcanis gb :	TGAATCAGG	AATGT	CACGGTGAATACGTTCCCGGGTC		: 1342
Hcinaedi g :	AATCAGG	AATGT	GCGGTGAATACGTTCCCGGGTC		: 1350
Hacinonych :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1355
Hnemestrin :	TATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1351
Hcholescys :	TGAATCAGG	TATGT	CACGGTGAATACGTTCCCGGGTC		: 1332
Hpamatensi :	TGAATCAGG	TATGT	CACGGTGAATACGTTCCCGGGTC		: 1352
Hmustelae :	TGAATCAGG	TATGT	CACGGTGAATACGTTCCCGGGTC		: 1352
Hrodentium :	TGATCAGG	TATGT	CACGGTGAATACGTTCCCGGGTC		: 1326
Hpullorum :	AATCAGG	TATGT	GCGGTGAATACGTTCCCGGGTC		: 1342
Hfennellia :	AATCAGG	AATGT	GCGGTGAATACGTTCCCGGGTC		: 1351
Htrogontum :	AATCAGG	AATGT	GCGGTGAATACGTTCCCGGGTC		: 1326
Hmuridarum :	TGAATCAGG	TATGT	CACGGTGAATACGTTCCCGGGTC		: 1348
Hhepaticus :	AATCAGG	TATGT	CACGGTGAATACGTTCCCGGGTC		: 1205
Abutzleri :	TGATCAGG	TATGT	CACGGTGAATACGTTCCCGGGTC		: 1367
Cjejuni gb :	TGATCAGG	TATGT	CACGGTGAATACGTTCCCGGGTC		: 1364
Wsuccinoge :	TGATCAGG	AATGT	CACGGTGAATACGTTCCCGGGTC		: 1352
	aATCAGC	ATGT	CGGTGAATACGTTCCCGGGTC		

Figure 2 - 42

```

      1560          *          1580          *
Hsuis2BXA0 : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1335
Ghominis1| : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1355
Ghominis2| : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1363
Hfelis|gb| : TTGTA1CTCACC2GC3HNCCGTCACACCATGGGAGTTGTGTT : 1386
Hbizzozero : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1362
Hbilis|gb| : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1559
Hsalomonis : TTGTA1CT----- : 1290
Hpylori|gb| : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1393
Hcanis|gb| : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1379
Hcinaedi|g : TTGTA1CTCACC2GC3NCGTCACACCATGGGAGTTGTGTT : 1387
Hacinonych : TTGTA1CTCACC2GC3NCGTCACACCATGGGAGTTGTGTT : 1392
Hnemestrin : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1388
Hcholescys : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1369
Hpamatensi : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1389
Hmustelae| : TTGTA1CTCACC2GC3NCGTCACACCATGGGAGTTGTGTT : 1389
Hrodentium : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1363
Hpullorum| : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1379
Hfennellia : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1388
Htrogontum : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1363
Hmuridarum : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1385
Hhepaticus : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1242
Abutzleri| : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGATCT : 1404
Cjejuni|gb : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGATTT : 1401
Wsuccinoge : TTGTA1CTCACC2GCCCGTCACACCATGGGAGTTGTGTT : 1389
TTGTA1CTcaccgcccgtcacaccatgggagttgt tt

```

Figure 2 - 43

```

              1600          *          1620
Hsuis2BXA0 : TGCCTTAAG CAG AT CTAAAGCAG TACTG CCAC : 1372
Ghominis1| : TGCCTTAAG CAG AT CTAAAGCAG TACTG CCAC : 1392
Ghominis2| : TGCCTTAAG CAG AT CTAAAGCAG TACTG CCAC : 1400
Hfelis|gb| : TGCCTTAAG CAG AT CTAAAGGTAG TACTG CCAC : 1423
Hbizzozero : TGCCTTAAG CAG AT CTAAAGTAG TACTG CCAC : 1399
Hbilis|gb| : GCCTTAAG C G ATACTAAATTGTTAC G CCAC : 1596
Hsalomonis : ----- : -
Hpylori|gb : TGCCTTAAG CAG AT CTAAATTGG TACTG CCAC : 1430
Hcanis|gb| : GCCTTAAG C G ATACTAAATTGGT----- : 1406
Hcinaedi|g : GCCTTAAG C G ATACTAAATTGGTTAN G CCAC : 1424
Hacinonych : TGCCTTAAG CAG AT CTAAAGCAG TACTG CCAC : 1429
Hnemestrin : TGCCTTAAG A G AT CTAAATTACGTACTG CCAC : 1425
Hcholescys : GCCTTAAGCC G AT CTAAACTGG TAC GTCCAC : 1406
Hpamatensi : GCCTTAAGCC G AT CTAAACTGG TAC GTCCAC : 1426
Hmustelae| : GCCTTAAGCC G AT CTAAATTGG TAC GTCCAC : 1426
Hrodentium : GCCTTAAG C GAAT CCAACTGG TAC G CCAC : 1400
Hpullorum| : GCCTTAAG C GAAT CCAACTAGTTAN N CCAC : 1416
Hfennellia : GCCCTAAGCC GAAT CTAAATTGG TAC GTCCAC : 1425
Htrogontum : GCCTTAAG C GAAT CCAACTGG TAC G CCAC : 1400
Hmuridarum : GCCTTAAG C G ATACTAAATTGTTAC G CCAC : 1422
Hhepaticus : GCCTTAAG C G ATACTAAATTGTTAC G CCAC : 1279
Abutzleri| : ATTTCGAAGCG G AT CTAAAGTAG TAC TTCCAC : 1441
Cjejuni|gb : ACTCGAAGCC G GAATCTAAACTAGTTAC GTCCAC : 1438
Wsuccinoge : GCCTTAAGCC G G AC CTAAACTGG TAC GTCCAC : 1426
gccttaag c g at ctaa t g tac g ccac

```

Figure 2 - 44

EP 1 035 219 A1

	*	1640	*	1660	
Hsuis2BXA0 :	GGCACACACAGCGACTGGGG	TGAAGTCGTAACAAGGT	:	1409	
Ghominis1 :	GGCACACACAGCGACTGGGG	TG-----	:	1414	
Ghominis2 :	GGCACACACAGCGACTGGGG	TG-----	:	1422	
Hfelis gb :	GGCACACACAGCGACTGGGG	-----	:	1443	
Hbizzozero :	GGCACACACAGCGACTGGGG	TG-----	:	1421	
Hbilis gb :	GGCAGATGCAGCGACTGGGG	-----	:	1616	
Hsalomonis :	-----	-----	:	-	
Hpylori gb :	GGCACACACAGCGACTGGGG	-----	:	1450	
Hcanis gb :	-----	-----	:	-	
Hcinaedi g :	GGCAGATGCAGCGACTGGGG	-----	:	1444	
Hacinonych :	GGCACACACAGCGACTGGGG	-----	:	1449	
Hnemestrin :	GGCACACACAGCGACTGGGG	TGAAGTCGTAACAAGGT	:	1462	
Hcholescys :	GGCAGATGCAGCGACTGGGG	-----	:	1425	
Hpamatensi :	GGCAGATGCAGCGACTGGGG	-----	:	1446	
Hmustelae :	GGCAGATNC-----	-----	:	1435	
Hrodentium :	GGCAGATGCAGCGACTGGGG	TGA-----	:	1423	
Hpullorum :	GGCAGATGCAGC-----	-----	:	1428	
Hfennellia :	GGCAGATGCAGCGACTGGGG	-----	:	1445	
Htrogontum :	GGCAGATGCAGCGACTGGGG	TG-----	:	1422	
Hmuridarum :	GGCAGATGCAGCGACTGGGG	-----	:	1442	
Hhepaticus :	GNCAGATGCAGCGACTGGGG	TGA-----	:	1302	
Abutzleri :	AGTCAATTGAGYACTGGGG	-----	:	1461	
Cjejuni gb :	AGTCAATTGAGCGACTGGGG	-----	:	1458	
Wsuccinoge :	GGCAGATGCAGCGACTGGGG	-----	:	1446	

ggc a cagcgactgggg

Figure 2 - 45

*

Hsuis2BXA0	:	AACCCGGGCGGC	:	1421
Ghominis1	:	-----	:	-
Ghominis2	:	-----	:	-
Hfelis gb	:	-----	:	-
Hbizzozero	:	-----	:	-
Hbilis gb	:	-----	:	-
Hsalomonis	:	-----	:	-
Hpylori gb	:	-----	:	-
Hcanis gb	:	-----	:	-
Hcinaedi g	:	-----	:	-
Hacinonych	:	-----	:	-
Hnemestrin	:	A-----	:	1463
Hcholescys	:	-----	:	-
Hpamatensi	:	-----	:	-
Hmustelae	:	-----	:	-
Hrodentium	:	-----	:	-
Hpullorum	:	-----	:	-
Hfennellia	:	-----	:	-
Htrogontum	:	-----	:	-
Hmuridarum	:	-----	:	-
Hhepaticus	:	-----	:	-
Abutzleri	:	-----	:	-
Cjejuni gb	:	-----	:	-
Wsuccinoge	:	-----	:	-

Figure 2 - 46

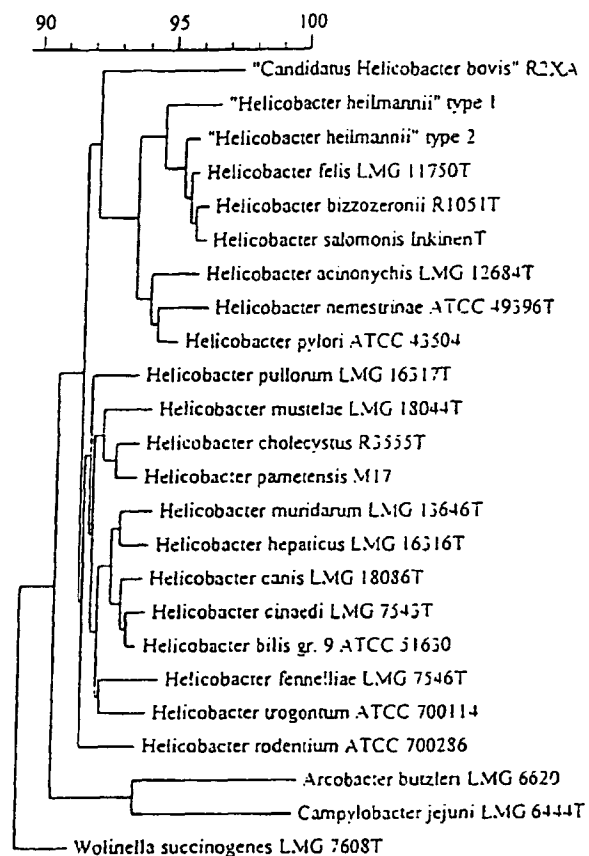


Fig 3A

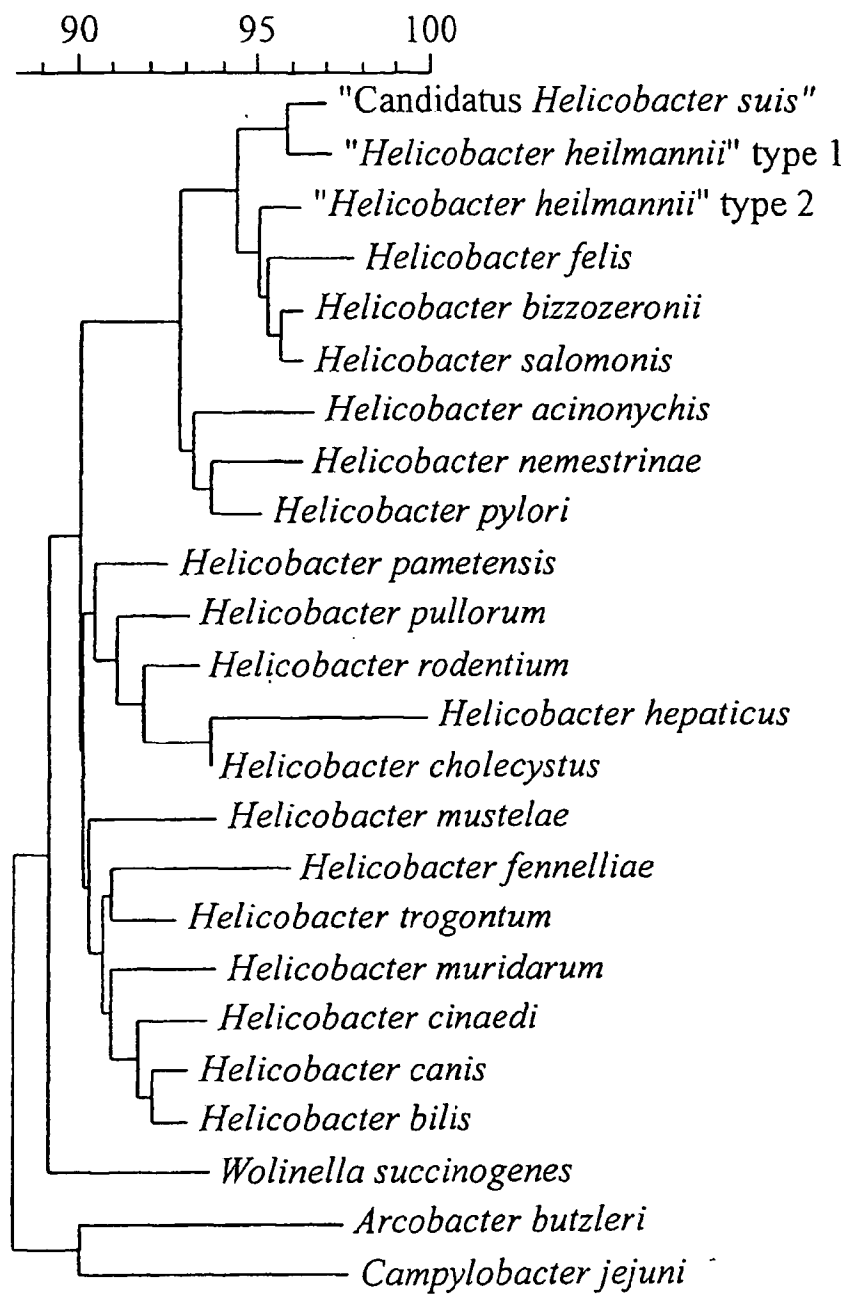


Fig 3B

R2XA001	ACGCTGGCGG	CGTGCCTAAT	ACATGCAAGT	CGAAGGATGA	AGTTTCGAGC
R5XE001	ACGCTGGCGG	CGTGCCTAAT	ACATGCAAGT	CGAAGGATGA	AGTTTCGAGC
R3XA001	ACGCTGGCGG	CGTGCCTAAT	ACATGCAAGT	CGAAGGATGA	AGTTTCGAGC
R6XA001
R13D001INV
R27TOTAAL
R28TOTAAL
R2XA001	TTGCTAGGAA	TGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R5XE001	TTGCTAGGAA	TGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R3XA001	TTGCTAGGAA	TGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R6XA001	TTGCTAGGAA	TGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R13D001INV	TTGCTAGGAA	TGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R27TOTAAL
R28TOTAAL
R2XA001	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R5XE001	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R3XA001	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R6XA001	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R13D001INV	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R27TOTAAL	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R28TOTAAL	CCCTTTAGTC	TGGGATAGCC	ACCGGAAAC	TGATTAATA	CTAGATACGC
R2XA001	CCTAAGGGGG	AAAGAATTTT	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R5XE001	CCTAAGGGGG	AAAGAATTTT	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R3XA001	CCTAAGGGGG	AAAGAATTTT	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R6XA001	CCTAAGGGGG	AAAGAATTTT	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R13D001INV	CCTAAGGGGG	AAAGAATTTT	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R27TOTAAL	CCTAAGGGGG	AAAGAATTTT	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R28TOTAAL	CCTAAGGGGG	AAAGAATTTT	GCTAAAGGAT	CAGCCTATGT	CCTATCAGCT
R2XA001	AGTTGGTGAG	GTAAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R5XE001	AGTTGGTGAG	GTAAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R3XA001	AGTTGGTGAG	GTAAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R6XA001	AGTTGGTGAG	GTAAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R13D001INV	AGTTGGTGAG	GTAAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R27TOTAAL	AGTTGGTGAG	GTAAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R28TOTAAL	AGTTGGTGAG	GTAAATGCTT	ACCAAGGCTA	TGACGGGTAT	CCGCTTGAG
R2XA001	AGGGTGAACG	GACACACCGG	AACTGAGACA	CGGTCCGGAC	TCCTACGGGA
R5XE001	AGGGTGAACG	GACACACCGG	AACTGAGACA	CGGTCCGGAC	TCCTACGGGA
R3XA001	AGGGTGAACG	GACACACCGG	AACTGAGACA	CGGTCCGGAC	TCCTACGGGA
R6XA001	AGGGTGAACG	GACACACCGG	AACTGAGACA	CGGTCCGGAC	TCCTACGGGA
R13D001INV	AGGGTGAACG	GACACACCGG	AACTGAGACA	CGGTCCGGAC	TCCTACGGGA
R27TOTAAL	AGGGTGAACG	GACACACCGG	AACTGAGACA	CGGTCCGGAC	TCCTACGGGA
R28TOTAAL	AGGGTGAACG	GACACACCGG	AACTGAGACA	CGGTCCGGAC	TCCTACGGGA

Figure 4 - 1

R2XA001	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTGA	AGCAGCAACG
R5XE001	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTGA	AGCAGCAACG
R3XA001	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTGA	AGCAGCAACG
R6XA001	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTGA	AGCAGCAACG
R13D001INV	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTGA	AGCAGCAACG
R27TOTAAL	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTGA	AGCAGCAACG
R28TOTAAL	GGCAGCAGTA	GGGAATATTG	CTCAATGGGG	GAAACCCCTGA	AGCAGCAACG
R2XA001	CCGCCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R5XE001	CCGCCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R3XA001	CCGCCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R6XA001	CCGCCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R13D001INV	CCGCCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R27TOTAAL	CCGCCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R28TOTAAL	CCGCCGTGGAG	GATGAAGGTT	CTAGGATTGT	AAACTCCTTT	TCTGAGAGAA
R2XA001	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R5XE001	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R3XA001	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R6XA001	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R13D001INV	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R27TOTAAL	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R28TOTAAL	GATAATGACC	GTATCTCAGG	AATAAGCACC	GGCTAACTCC	GTGCCAGCA
R2XA001	CCGCCGTAAT	ACGGAGGGTG	CAACCGTTAC	TCGGAATCAC	TGGGCGTAAA
R5XE001	CCGCCGTAAT	ACGGAGGGTG	CAACCGTTAC	TCGGAATCAC	TGGGCGTAAA
R3XA001	CCGCCGTAAT	ACGGAGGGTG	CAACCGTTAC	TCGGAATCAC	TGGGCGTAAA
R6XA001	CCGCCGTAAT	ACGGAGGGTG	CAACCGTTAC	TCGGAATCAC	TGGGCGTAAA
R13D001INV	CCGCCGTAAT	ACGGAGGGTG	CAACCGTTAC	TCGGAATCAC	TGGGCGTAAA
R27TOTAAL	CCGCCGTAAT	ACGGAGGGTG	CAACCGTTAC	TCGGAATCAC	TGGGCGTAAA
R28TOTAAL	CCGCCGTAAT	ACGGAGGGTG	CAACCGTTAC	TCGGAATCAC	TGGGCGTAAA
R2XA001	GAGCGTGTAG	GCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAC
R5XE001	GAGCGTGTAG	GCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAC
R3XA001	GAGCGTGTAG	GCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAC
R6XA001	GAGCGTGTAG	GCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAC
R13D001INV	GAGCGTGTAG	GCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAC
R27TOTAAL	GAGCGTGTAG	GCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAC
R28TOTAAL	GAGCGTGTAG	GCGGAATGAT	AAGTCAGGCG	TGAAATCCCG	TGGCTTAAC
R2XA001	GCGGAAGTGC	GTTTGAAACT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R5XE001	GCGGAAGTGC	GTTTGAAACT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R3XA001	GCGGAAGTGC	GTTTGAAACT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R6XA001	GCGGAAGTGC	GTTTGAAACT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R13D001INV	GCGGAAGTGC	GTTTGAAACT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R27TOTAAL	GCGGAAGTGC	GTTTGAAACT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG
R28TOTAAL	GCGGAAGTGC	GTTTGAAACT	ATCATTCTGG	AGTGTGGGAG	AGGCAGGTGG

Figure 4 - 2

R2XA001	A A C T C T T G G T	G T A G G G G T A A	A A T C C G T A G A	T A T C A A G A A G	A A T A C T C A T T
R5XE001	A A C T C T T G G T	G T A G G G G T A A	A A T C C G T A G A	T A T C A A G A A G	A A T A C T C A T T
R3XA001	A A C T C T T G G T	G T A G G G G T A A	A A T C C G T A G A	T A T C A A G A A G	A A T A C T C A T T
R6XA001	A A C T C T T G G T	G T A G G G G T A A	A A T C C G T A G A	T A T C A A G A A G	A A T A C T C A T T
R13D001 INV	A A C T C T T G G T	G T A G G G G T A A	A A T C C G T A G A	T A T C A A G A A G	A A T A C T C A T T
R27T0TAAL	A A C T C T T G G T	G T A G G G G T A A	A A T C C G T A G A	T A T C A A G A A G	A A T A C T C A T T
R28T0TAAL	A A C T C T T G G T	G T A G G G G T A A	A A T C C G T A G A	T A T C A A G A A G	A A T A C T C A T T

R2XA001	GCGAAGGC	A	CCTGCTGGAA	CAT	ACTGAC	GCTGATGCCG	GAAAGC	TGG
R5XE001	GCGAAGGC	A	CCTGCTGGAA	CAT	ACTGAC	GCTGATGCCG	GAAAGC	TGG
R3XA001	GCGAAGGC	A	CCTGCTGGAA	CAT	ACTGAC	GCTGATGCCG	GAAAGC	TGG
R6XA001	GCGAAGGC	A	CCTGCTGGAA	CAT	ACTGAC	GCTGATGCCG	GAAAGC	TGG
R13D001INV	GCGAAGGC	A	CCTGCTGGAA	CAT	ACTGAC	GCTGATGCCG	GAAAGC	TGG
R27TOTAAL	GCGAAGGC	A	CCTGCTGGAA	CAT	ACTGAC	GCTGATGCCG	GAAAGC	TGG
R28TOTAAL	GCGAAGGC	A	CCTGCTGGAA	CAT	ACTGAC	GCTGATGCCG	GAAAGC	TGG

R2XA001	GG	AGCAAAC	AGGATTAGAT	ACCCTGGTAG	TCCACGCCCT	AAACGATGGA
R5XE001	GG	AGCAAAG	AGGATTAGAT	ACCCTGGTAG	TCCACGCCCT	AAACGATGGA
R3XA001	GG	AGCAAAC	AGGATTAGAT	ACCCTGGTAG	TCCACGCCCT	AAACGATGGA
R6XA001	GG	AGCAAAC	AGGATTAGAT	ACCCTGGTAG	TCCACGCCCT	AAACGATGGA
R13D001INV	GG	AGCAAAC	AGGATTAGAT	ACCCTGGTAG	TCCACGCCCT	AAACGATGGA
R27T0TAAL	GG	AGCAAAC	AGGATTAGAT	ACCCTGGTAG	TCCACGCCCT	AAACGATGGA
R28T0TAAL	GG	AGCAAAC	AGGATTAGAT	ACCCTGGTAG	TCCACGCCCT	AAACGATGGA

R2XA001	TGCTAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT-AGCT	AACGCATTAA
R5XE001	TGCTAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT-AGCT	AACGCATTAA
R3XA001	TGCTAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT-AGCT	AACGCATTAA
R6XA001	TGCTAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT-AGCT	AACGCATTAA
R13D001INV	TGCTAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT-AGCT	AACGCATTAA
R27TOTAL	TGCTAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT-AGCT	AACGCATTAA
R28TOTAL	TGCTAATTGT	CGGGGGGCTT	GTCTCCTCGG	TAAT-AGCT	AACGCATTAA

R2XA001	GATCCCGCC	TGGGGAGTAC	GATCGCAAGA	TTAAAACTCA	AAGGAATAGA
R5XE001	GATCCCGCC	TGGGGAGTAC	GATCGCAAGA	TTAAAACTCA	AAGGAATAGA
R3XA001	GATCCCGCC	TGGGGAGTAC	GATCGCAAGA	TTAAAACTCA	AAGGAATAGA
R6XA001	GATCCCGCC	TGGGGAGTAC	GATCGCAAGA	TTAAAACTCA	AAGGAATAGA
R13D001INV	GATCCCGCC	TGGGGAGTAC	GATCGCAAGA	TTAAAACTCA	AAGGAATAGA
R27TOTAAL	GATCCCGCC	TGGGGAGTAC	GATCGCAAGA	TTAAAACTCA	AAGGAATAGA
R28TOTAAL	GATCCCGCC	TGGGGAGTAC	GATCGCAAGA	TTAAAACTCA	AAGGAATAGA

R2XA001	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAATTCC	AAGATACGCC
R5XE001	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAATTCC	AAGATACGCC
R3XA001	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAATTCC	AAGATACGCC
R6XA001	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAATTCC	AAGATACGCC
R13D001INV	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAATTCC	AAGATACGCC
R27TOTAAL	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAATTCC	AAGATACGCC
R28TOTAAL	CGGGGACCCG	CACAAGCGGT	GGAGCATGTG	GTTTAATTCC	AAGATACGCC

Figure 4 - 3

R2XA001	AAGAACCTTA	CCCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGGA
R5XE001	AAGAACCTTA	CCCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGGA
R3XA001	AAGAACCTTA	CCCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGGA
R6XA001	AAGAACCTTA	CCCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGGA
R13D001INV	AAGAACCTTA	CCCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGGA
R27TOTAAL	AAGAACCTTA	CCCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGGA
R28TOTAAL	AAGAACCTTA	CCCAGGCTTG	ACATTGATG	AATCTACCC	AAAAGGTGGA
R2XA001	GTGCCAGTTT	ACTGGAGCCT	GAAAACAGGT	GCTGCACGGC	TGTCGTCAGC
R5XE001	GTGCCAGTTT	ACTGGAGCCT	GAAAACAGGT	GCTGCACGGC	TGTCGTCAGC
R3XA001	GTGCCAGTTT	ACTGGAGCCT	GAAAACAGGT	GCTGCACGGC	TGTCGTCAGC
R6XA001	GTGCCAGTTT	ACTGGAGCCT	GAAAACAGGT	GCTGCACGGC	TGTCGTCAGC
R13D001INV	GTGCCAGTTT	ACTGGAGCCT	GAAAACAGGT	GCTGCACGGC	TGTCGTCAGC
R27TOTAAL	GTGCCAGTTT	ACTGGAGCCT	GAAAACAGGT	GCTGCACGGC	TGTCGTCAGC
R28TOTAAL	GTGCCAGTTT	ACTGGAGCCT	GAAAACAGGT	GCTGCACGGC	TGTCGTCAGC
R2XA001	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AACCCCTCGTC
R5XE001	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AACCCCTCGTC
R3XA001	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AACCCCTCGTC
R6XA001	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AACCCCTCGTC
R13D001INV	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AACCCCTCGTC
R27TOTAAL	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AACCCCTCGTC
R28TOTAAL	TCGTGTCGTG	AGATGTTGGG	TTAAGTCCCG	CAACGAGCGC	AACCCCTCGTC
R2XA001	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R5XE001	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R3XA001	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R6XA001	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R13D001INV	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R27TOTAAL	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R28TOTAAL	CTTAGTTGCC	ATCAGTTCGG	CTGGGCACTC	TAAGGAGACT	GCCTTCGTAA
R2XA001	GGAGGAGGAA	GGCGAGGATG	ACGTCAAGTC	ATC . ATGGCC	C . TTA T G C
R5XE001	GGAGGAGGAA	GGCGAGGATG	ACGTCAAGTC	ATC . ATGGCC	C . TTA G C
R3XA001	GGAGGAGGAA	GGCGAGGATG	ACGTCAAGTC	ATC . ATGGCC	C . TTA G C
R6XA001	GGAGGAGGAA	GGCGAGGATG	ACGTCAAGTC	ATC . ATGGCC	C . TTA G C
R13D001INV	GGAGGAGGAA	GGCGAGGATG	ACGTCAAGTC	ATC . ATGGCC	C . TTA G C
R27TOTAAL	GGAGGAGGAA	GGCGAGGATG	ACGTCAAGTC	ATC . ATGGCC	C . TTA G C
R28TOTAAL	GGAGGAGGAA	GGCGAGGATG	ACGTCAAGTC	ATC . ATGGCC	C . TTA G C
R2XA001	GGGGCTACCC	ACGTGCTACA	ATGGGATGTA	CAAAGAGATG	CAATGTCGTA
R5XE001	GGGGCTACCC	ACGTGCTACA	ATGGGATGTA	CAAAGAGATG	CAATGTCGTA
R3XA001	GGGGCTACCC	ACGTGCTACA	ATGGGATGTA	CAAAGAGATG	CAATGTCGTA
R6XA001	GGGGCTACCC	ACGTGCTACA	ATGGGATGTA	CAAAGAGATG	CAATGTCGTA
R13D001INV	GGGGCTACCC	ACGTGCTACA	ATGGGATGTA	CAAAGAGATG	CAATGTCGTA
R27TOTAAL	GGGGCTACCC	ACGTGCTACA	ATGGGATGTA	CAAAGAGATG	CAATGTCGTA
R28TOTAAL	GGGGCTACCC	ACGTGCTACA	ATGGGATGTA	CAAAGAGATG	CAATGTCGTA

Figure 4 - 4

R2XA001	AGATGGAGCA	AAACTCAAAA	AGATCTCCCA	GTTCCGATTG	TGGTCTGCAA
R5XE001	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCCGATTG	TGGTCTGCAA
R3XA001	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCCGATTG	TGGTCTGCAA
R6XA001	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCCGATTG	TGGTCTGCAA
R13D001INV	AGATGGAGCA	AAACTCAAAA	CGRTCTCCCA	GTTCCGATTG	TGGTCTGCAA
R27TOTAAL	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCCGATTG	TGGTCTGCAA
R28TOTAAL	AGATGGAGCA	AAACTCAAAA	ATCTCCCA	GTTCCGATTG	TGGTCTGCAA

R2XA001	CTCGACCACA	TG	CTCGACCACA	ATCGGATG	ATCGGATG	ATCGGATG
R5XE001	CTCGACCACA	TG	CTCGACCACA	ATCGGATG	ATCGGATG	ATCGGATG
R3XA001	CTCGACCACA	TG	CTCGACCACA	ATCGGATG	ATCGGATG	ATCGGATG
R6XA001	CTCGACCACA	TG	CTCGACCACA	ATCGGATG	ATCGGATG	ATCGGATG
R13D001INV	CTCGACCACA	TG	CTCGACCACA	ATCGGATG	ATCGGATG	ATCGGATG
R27TOTAAL	CTCGACCACA	TG	CTCGACCACA	ATCGGATG	ATCGGATG	ATCGGATG
R28TOTAAL	CTCGACCACA	TG	CTCGACCACA	ATCGGATG	ATCGGATG	ATCGGATG

R2XA001	GGGTGAATAC	GTTCCCGGGT	CTTGACTCA	CCAATCAC	1335
R5XE001	GGGTGAATAC	GTTCCCGGGT	CTTGACTCA	CCAA...	1331
R3XA001	GG				1299
R6XA001	G				1267
R13D001INV					1236
R27TOTAAL					1194
R28TOTAAL					1172

Figure 4 - 5

EP 1 035 219 A1

	1				50
2BXA001	TGCAAGTCGA	ACGATGAAGC	CTAGCTTGCT	AGGTTTAA	GTGGCGCACG
4AXA001	TGCAAGTCGA	ACGATGAAGC	CTAGCTTGCT	AGGTTTAA	GTGGCGCACG
6W06001	GTGGCGCACG
V14D001	GTGGCGCACG
V19DINV001	GTGDHGCACG
	51				100
2BXA001	GGTGAGTAAT	GCATAGATGA	CATGCCCTTT	AGTTTGGAAT	AGCCACTAGA
4AXA001	GGTGAGTAAT	GCATAGATGA	CATGCCCTTT	AGTTTGGAAT	AGCCACTAGA
6W06001	GGTGAGTAAT	GCATAGATGA	CATGCCCTTT	AGTTTGGAAT	AGCCACTAGA
V14D001	GGTGAGTAAT	GCATAGATGA	CATGCCCTTT	AGTTTGGAAT	AGCCACTAGA
V19DINV001	GGTGAGTAAT	GCATAGATGA	CATGCCCTTT	AGTTTGGAAT	AGCCACTAGA
	101				150
2BXA001	AATGGTGAT	TAATACCAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT
4AXA001	AATGGTGAT	TAATACCAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT
6W06001	AATGGTGAT	TAATACCAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT
V14D001	AATGGTGAT	TAATACCAA	TACTACCTTA	CGAGGGAAAG	ATTATCGCT
V19DINV001	AATGGTGAT	TAATACCAA	TACTACCTTA	CGAGGGVNA	ATTATCGCT
	151				200
2BXA001	AAAGCATTGG	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC
4AXA001	AAAGCATTGG	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC
6W06001	AAAGCATTGG	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC
V14D001	AAAGCATTGG	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC
V19DINV001	AAAGCATTGG	TCTATGTCCT	ATCAGCTTGT	TGGTGAGGT	AAAGGCTCAC
	201				250
2BXA001	CAAGGCTAT	GACGGGTATC	CGGCCTGAGA	GGGTGAGCGG	ACACACTGGA
4AXA001	CAAGGCTAT	GACGGGTATC	CGGCCTGAGA	GGGTGAGCGG	ACACACTGGA
6W06001	CAAGGCTAT	GACGGGTATC	CGGCCTGAGA	GGGTGAGCGG	ACACACTGGA
V14D001	CAAGGCTAT	GACGGGTATC	CGGCCTGAGA	GGGTGAGCGG	ACACACTGGA
V19DINV001	CAAGGCTAT	GACGGGTATC	CGGCCTGAGA	GGGTGAGCGG	ACACACTGGA
	251				300
2BXA001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC
4AXA001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC
6W06001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC
V14D001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC
V19DINV001	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTAG	GGAATATTGC
	301				350
2BXA001	TCAATGGGGG	AAACCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT
4AXA001	TCAATGGGGG	AAACCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT
6W06001	TCAATGGGGG	AAACCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT
V14D001	TCAATGGGGG	AAACCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT
V19DINV001	TCAATGGGGG	AAACCCTGA	AGCAGCAACG	CCGCGTGGAG	GATGAAGGTT
	351				400
2BXA001	TTAGGATCGT	AAACTCCTTT	TGTTAGAGAA	GATAATGACC	GTATCTAACG
4AXA001	TTAGGATCGT	AAACTCCTTT	TGTTAGAGAA	GATAATGACC	GTATCTAACG
6W06001	TTAGGATCGT	AAACTCCTTT	TGTTAGAGAA	GATAATGACC	GTATCTAACG
V14D001	TTAGGATCGT	AAACTCCTTT	TGTTAGAGAA	GATAATGACC	GTATCTAACG
V19DINV001	TTAGGATCGK	AAACTCCTTT	TGTTAGAGAA	GATAATGACC	GTATCTAACG

Figure 5 - 1

	401				450
2BXA001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCCGTAAT	ACGGAGGGTG
4AXA001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCCGTAAT	ACGGAGGGTG
6W06001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCCGTAAT	ACGGAGGGTG
V14D001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCCGTAAT	ACGGAGGGTG
V19DINV001	AATAAGCACC	GGCTAACTCC	GTGCCAGCAG	CCGCCGTAAT	ACGGAGGGTG
	451				500
2BXA001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	GCGGGCAGGA
4AXA001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	GCGGGCAGGA
6W06001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	GCGGGCAGGA
V14D001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	GCGGGCAGGA
V19DINV001	CAAGCGTTAC	TCGGAATCAC	TGGGCGTAA	GAGTGCCTAG	GCGGGCAGGA
	501				550
2BXA001	CAAGTCAGGT	GTG...AAATC	CTATGG...CTT	AACCATAGAA	CTGCATTTGA
4AXA001	CAAGTCAGGT	GTG...AAATC	CTATGG...CTT	AACCATAGAA	CTGCATTTGA
6W06001	CAAGTCAGGT	GTG...AAATC	CTATGG...CTT	AACCATAGAA	CTGCATTTGA
V14D001	CAAGTCAGGT	GTG...AAATC	CTATGG...CTT	AACCATAGAA	CTGCATTTGA
V19DINV001	CAAGTCAGGT	GTG...AAATC	CTATGG...CTT	AACCATAGAA	CTGCATTTGA
	551				600
2BXA001	AACTATCCTT	CTGGAGTGTG	GGGAGGTTAG	GTGGAATTCT	TGGTGTAGGG
4AXA001	AACTATCCTT	CTGGAGTGTG	GGGAGGTTAG	GTGGAATTCT	TGGTGTAGGG
6W06001	AACTATCCTT	CTGGAGTGTG	GGGAGGTTAG	GTGGAATTCT	TGGTGTAGGG
V14D001	AACTATCCTT	CTGGAGTGTG	GGGAGGTTAG	GTGGAATTCT	TGGTGTAGGG
V19DINV001	AACTATCCTT	CTGGAGTGTG	GGGAGGTTAG	GTGGAATTCT	TGGTGTAGGG
	601				650
2BXA001	GGTAAATCC	GTAGAGATCA	AGAGGATAC	CATTG...CGA	AGGCGACCTG
4AXA001	GGTAAATCC	GTAGAGATCA	AGAGGATAC	CATTG...CGA	AGGCGACCTG
6W06001	G...TAAATCC	GTAGAGATCA	AGAGGATAC	CATTG...CGA	AGGCGACCTG
V14D001	G...TAAATCC	GTAGAGATCA	AGAGGATAC	CATTG...CGA	AGGCGACCTG
V19DINV001	G...TAAATCC	GTAGAGATCA	AGAGGATAC	CATTG...CGA	AGGCGACCTG
	651				700
2BXA001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
4AXA001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
6W06001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
V14D001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
V19DINV001	CTGGAACATC	ACTGACGCTG	ATTGCACGAA	AGCGTGGGG	AGCAAAACAGG
	701				750
2BXA001	ATTAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
4AXA001	ATTAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
6W06001	ATTAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
V14D001	ATTAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
V19DINV001	ATTAGATAC	CCTGGTAGTC	CACGCCCTAA	ACGAT...GGAT	GCTAGTTGTT
	751				800
2BXA001	GGGA...GGCTT	TGTCTTTCCA	GTAATGCAGS	TATCGCCTTA	AGCATCCCGC
4AXA001	GGGA...GGCTT	TGTCTTTCCA	GTAATGCAGC	TATCGCCTTA	AGCATCCCGC
6W06001	GGGA...GGCTT	TGTCTTTCCA	GTAATGCAGC	TATCGCCTTA	AGCATCCCGC
V14D001	GGGA...GGCTT	TGTCTTTCCA	GTAATGCAGC	TATCGCCTTA	AGCATCCCGC
V19DINV001	GGGA...GGCTT	TGTCTTTCCA	GTAATGCAGC	TATCGCCTTA	AGCATCCCGC

Figure 5 - 2

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	801				850	
2BXA001	CTGGGGAGTA	CGGTCGCAAG	ATTAAAACTC	AAAGG	AATA	GACGGGGACC
4AXA001	CTGGGGAGTA	CGGTCGCAAG	ATTAAAACTC	AAAGG	AATA	GACGGGGACC
6W06001	CTGGGGAGTA	CGGTCGCAAG	ATTAAAACTC	AAAGG	AATA	GACGGGGACC
V14D001	CTGGGGAGTA	CGGTCGCAAG	ATTAAAACTC	AAAGG	AATA	GACGGGGACC
V19DINV001	CTGGGGAGTA	CGGTCGCAAG	ATTAAAACTC	AAARG	GAATA	GACGGGGACC
	851				900	
2BXA001	CGCACAAAGCG	GTGGAGCATG	TGGTTTAATT	CGAGG	TACA	CGAAGAACC
4AXA001	CGCACAAAGCG	GTGGAGCATG	TGGTTTAATT	CGAGG	TACA	CGAAGAACC
6W06001	CGCACAAAGCG	GTGGAGCATG	TGGTTTAATT	CGAGG	TACA	CGAAGAACC
V14D001	CGCACAAAGCG	GTGGAGCATG	TGGTTTAATT	CGAGG	TACA	CGAAGAACC
V19DINV001	CGCACAAAGCG	GTGGAGCATG	TGGTTTAATT	CGAGG	TACA	CGAAGAACC
	901				950	
2BXA001	TTACCTAGGC	TTGACATTG	AAGGAATTCC	C	TAGAAATA	GGGGAGTGTG
4AXA001	TTACCTAGGC	TTGACATTG	AAGGAATTCC	C	TAGAAATA	GGGGAGTGTG
6W06001	TTACCTAGGC	TTGACATTG	AAGGAATTCC	C	TAGAAATA	GGGGAGTGTG
V14D001	TTACCTAGGC	TTGACATTG	AAGGAATTCC	C	TAGAAATA	GGGGAGTGTG
V19DINV001	TTACCTAGGC	TTGACATTG	AAGGAATTCC	C	TAGAAATA	GGGGAGTGTG
	951				1000	
2BXA001	TAGCTTGCTA	GACCCTGAAA	ACAGGTGCTG	CACGGCTGTC		GTCAGCTCGT
4AXA001	TAGCTTGCTA	GACCCTGAAA	ACAGGTGCTG	CACGGCTGTC		GTCAGCTCGT
6W06001	TAGCTTGCTA	GACCCTGAAA	ACAGGTGCTG	CACGGCTGTC		GTCAGCTCGT
V14D001	TAGCTTGCTA	GACCCTGAAA	ACAGGTGCTG	CACGGCTGTC		GTCAGCTCGT
V19DINV001	TAGCTTGCTA	GACCCTGAAA	ACAGGTGCTG	CACGGCTGTC		GTCAGCTCGT
	1001				1050	
2BXA001	GTCGTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
4AXA001	GTCGTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
6W06001	GTCGTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
V14D001	GTCGTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
V19DINV001	GTCGTGAGAT	GTTGGGTAA	GTCCCGCAAC	GAGCGCAACC	C	TTTTTCTT
	1051				1100	
2BXA001	AGTTGCTAAC	AGGTT	GCGCACTCTA	AGAAGACTGC		CTGCGTAAGC
4AXA001	AGTTGCTAAC	AGGTT	GCGCACTCTA	AGAAGACTGC		CTGCGTAAGC
6W06001	AGTTGCTAAC	AGGTT	GCGCACTCTA	AGAAGACTGC		CTGCGTAAGC
V14D001	AGTTGCTAAC	AGGTT	GCGCACTCTA	AGAAGACTGC		CTGCGTAAGC
V19DINV001	AGTTGCTAAC	AGGTT	GCGCACTCTA	AGAAGACTGC		CTGCGTAAGC
	1101				1150	
2BXA001	AGGAGGAAGG	TGAGGACGAC	GTCAAGTCAT	CATGGCCCTT		ACGCCTAGGG
4AXA001	AGGAGGAAGG	TGAGGACGAC	GTCAAGTCAT	CATGGCCCTT		ACGCCTAGGG
6W06001	AGGAGGAAGG	TGAGGACGAC	GTCAAGTCAT	CATGGCCCTT		ACGCCTAGGG
V14D001	AGGAGGAAGG	TGAGGACGAC	GTCAAGTCAT	CATGGCCCTT		ACGCCTAGGG
V19DINV001	AGGAGGAAGG	TGAGGACGAC	GTCAAGTCAT	CATGGCCCTT		ACGCCTAGGG
	1151				1200	
2BXA001	CTACACACGT	GCTACAATGG	GGTGACACAA	GAGATGCAAA		GCCGCGAGGC
4AXA001	CTACACACGT	GCTACAATGG	GGTGACACAA	GAGATGCAAA		GCCGCGAGGC
6W06001	CTACACACGT	GCTACAATGG	GGTGACACAA	GAGATGCAAA		GCCGCGAGGC
V14D001	CTACACACGT	GCTACAATGG	GGTGACACAA	GAGATGCAAA		GCCGCGAGGC
V19DINV001	CTACACACGT	GCTACAATGG	GGTGACACAA	GAGATGCAAA		GCCGCGAGGC

Figure 5 - 3

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	1201				1250	
2BXA001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG	
4AXA001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG	
6W06001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG	
V14D001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG	
V19DINV001	AGAGCTAATC	TATAAAACAC	CTCCTAGTTC	GGATTGCAGG	CTGCAACTCG	
	1251				1300	
2BXA001	CCTGCATGAA	GCTGGAAT.C	GCTAGTAA.T	CGCAAA.TCA	GCTATGTTGC	
4AXA001	CCTGCATGAA	GCTGGAAT.C	GCTAGTAA.T	CGCAAA.TCA	GCTATGTTGC	
6W06001	CCTGCATGAA	GCTGGAAT.C	GCTAGTAA.T	CGCAAA.TCA	GCTATGTTGC	
V14D001	CCTGCATGAA	GCTGGAAT.C	GCTAGTAA.T	CGCAAAATCA	GCTATGTTGC	
V19DINV001	CCTGCATGAA	GCTGGAATTC	GCTAGTAAAT	CGCAAAATCA	GCTATGTTGC	
	1301				1350	
2BXA001	GGTGAATA.C	GTTCCC.GGG	TCTTGACTC	ACCGCCC.GT	CACACC.ATG	
4AXA001	GGTGAATA.C	GTTCCC.GGG	TCTTGACTC	ACCGCCC.GT	CACACC.ATG	
6W06001	GGTGAATNAC	GTKCCC.GGG	TCTTGACTC	ACCGCCC.GT	CACACC.ATG	
V14D001	GGTGAATA.C	GTTCCC.CGG	TCTTGACTC	ACCGCCCCGT	CACACC.ATG	
V19DINV001	GGTGAATD.M	GTKCCCCGGG	TCTTGACTC	ACCGCCCCGT	CACACC.ATG	
	1351				1400	
2BXA001	GGAGTTGTGT	TTGCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCCACGG	
4AXA001	GGAGTTGTGT	TTGCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCCACGG	
6W06001	GGAGTTGTGT	TTGCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCCACG.	
V14D001	GGAGTTGTGT	TTGCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCCACG.	
V19DINV001	GGAGTTGTGT	TTGCCTTAAG	TCAGGATGCT	AAAGCAGCTA	CTGCCCACG.	
	1401			1447		
2BXA001	CACACACAGC	ACTGGGGTG	AAGTCGTAAC	AAGGTAACCC	GGGCGGC	1423
4AXA001	CACACACAGC	ACTGGGGTG	1400
6W06001	CACACACAGC	1353
V14D001	CACACACAGC	1355
V19DINV001	CACACACAGC	1358

Figure 5 - 4



European Patent
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EUROPEAN SEARCH REPORT

Application Number
EP 99 87 0035

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION
X	PASTER ET AL.: "Phylogeny of <i>Helicobacter felis</i> sp. nov., <i>Helicobacter mustelae</i> , and related bacteria." INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, vol. 41, no. 1, January 1991 (1991-01), pages 31-38, XP002110981 * the whole document *	1-10	C12Q1/68 A61K31/70
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-The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 4 August 1999	Examiner Reuter, U
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